Biological Databases: Information Retrieval

David Landsman

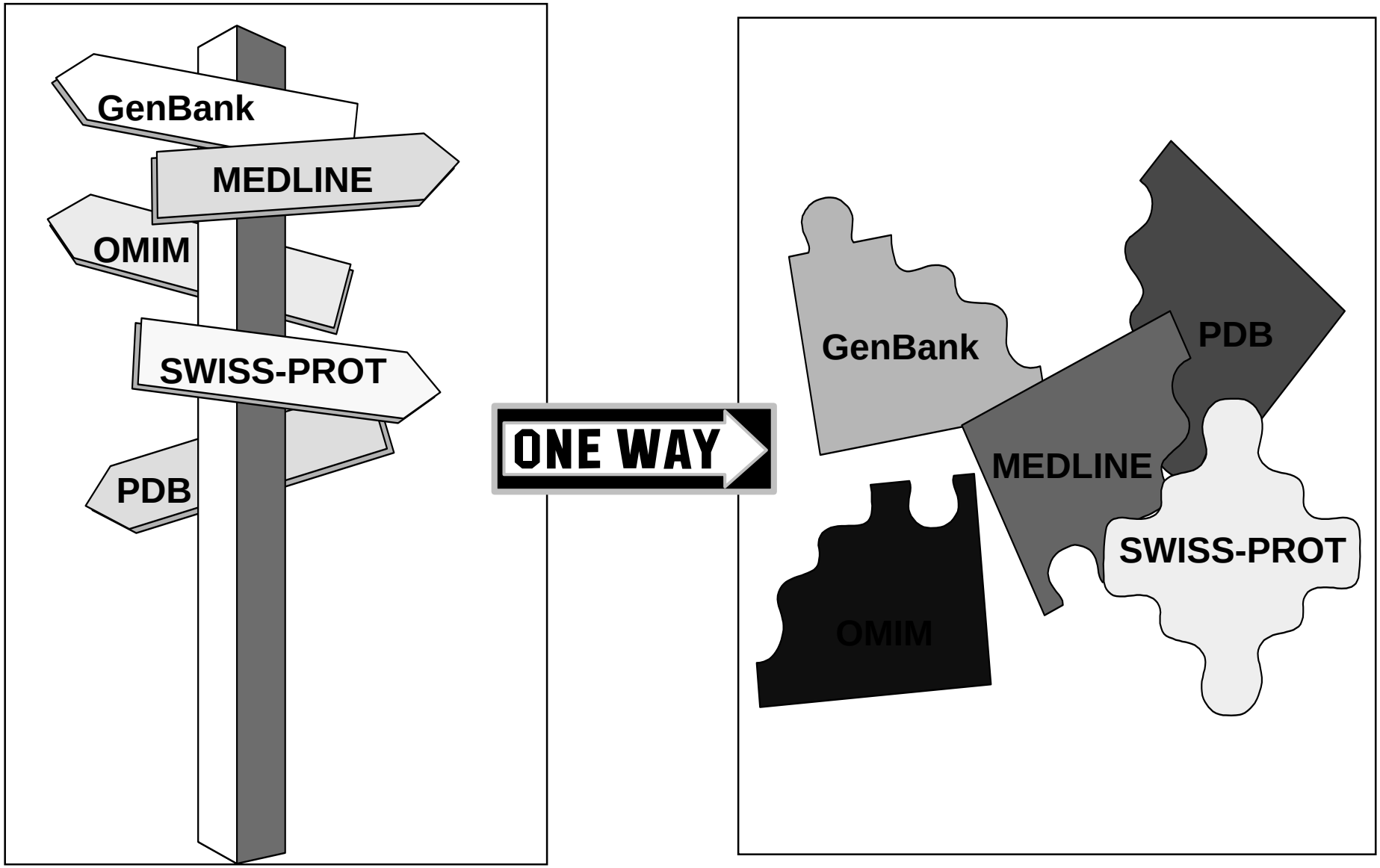
Computational Biology Branch

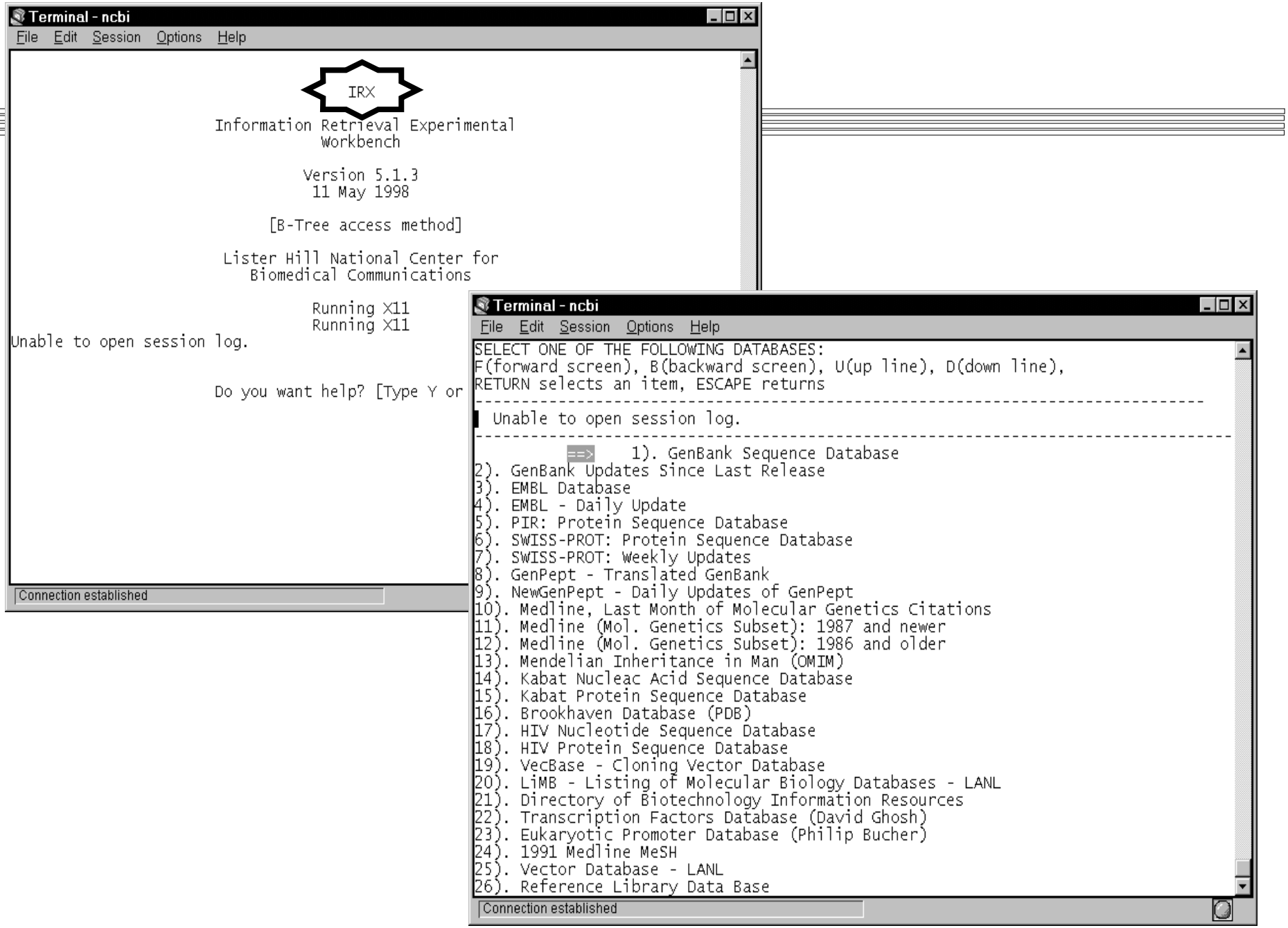
NCBI

How much information is there?

- Nucleotide records
  - 9,102,634
- Nucleotides
  - 10,335,692,655
- Protein sequences
  - 1,183,833
- 3D structures
  - 12,863
- Expression data points
  - >20,000,000
- Human Unigene clusters
  - 84,130
- Maps and complete genomes
  - 11,166
- Different taxonomy nodes
  - 162,025
- dbSNP
  - 1,463,178
- Human Refgene records
  - 14,133
- Human contigs >500 kb (28,525 MB)
  - 257
- PubMed records
  - 10,965,353
- OMIM records
  - 11,950

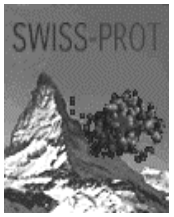
Information puzzles end abruptly?



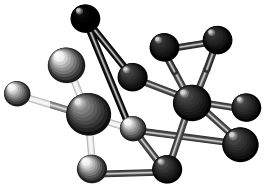

Terminal - ncbi
File Edit Session Options Help
IRX
Information Retrieval Experimental
Workbench
Version 5.1.3
11 May 1998
[B-Tree access method]
Lister Hill National Center for
Biomedical Communications
Running X11
Running X11
Unable to open session log.
Do you want help? [Type Y or
Connection established
Terminal - ncbi
File Edit Session Options Help
SELECT ONE OF THE FOLLOWING DATABASES:
F(forward screen), B(backward screen), U(up line), D(down line),
RETURN selects an item, ESCAPE returns
Unable to open session log.
==> 1). GenBank Sequence Database
2). GenBank Updates Since Last Release
3). EMBL Database
4). EMBL - Daily Update
5). PIR: Protein Sequence Database
6). SWISS-PROT: Protein Sequence Database
7). SWISS-PROT: Weekly Updates
8). GenPept - Translated GenBank
9). NewGenPept - Daily Updates of GenPept
10). Medline, Last Month of Molecular Genetics Citations
11). Medline (Mol. Genetics Subset): 1987 and newer
12). Medline (Mol. Genetics Subset): 1986 and older
13). Mendelian Inheritance in Man (OMIM)
14). Kabat Nucleac Acid Sequence Database
15). Kabat Protein Sequence Database
16). Brookhaven Database (PDB)
17). HIV Nucleotide Sequence Database
18). HIV Protein Sequence Database
19). VecBase - Cloning Vector Database
20). LiMB - Listing of Molecular Biology Databases - LANL
21). Directory of Biotechnology Information Resources
22). Transcription Factors Database (David Ghosh)
23). Eukaryotic Promoter Database (Philip Bucher)
24). 1991 Medline MeSH
25). Vector Database - LANL
26). Reference Library Data Base
Connection established

Vertical querying

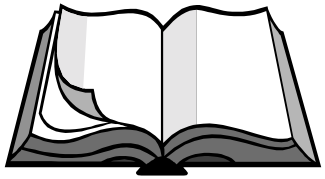
GenBank



SWISS-PROT



PDB

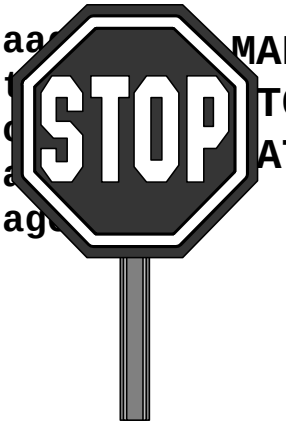


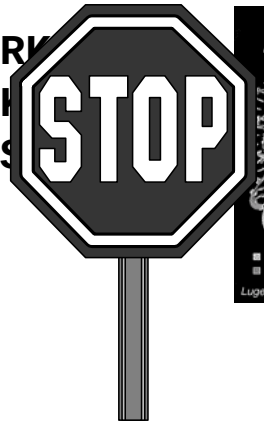
MEDLINE

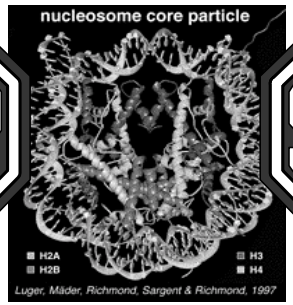
query query query query

```
atg gcc cga acc aa
act gct cgt aag t
ggt ggg aaa gcc c
aaa cag ctg gcc a
gcc gcc agg aaa ag
```

MARTKQTARK
TGGKAPRK
ATKAARKS





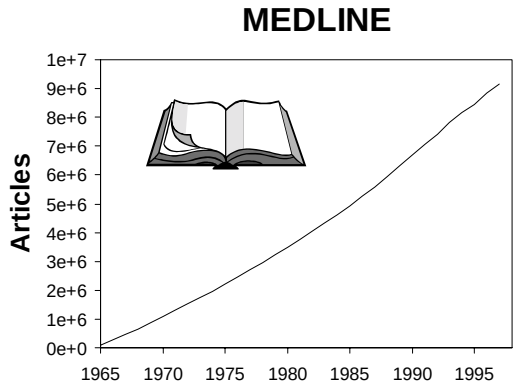


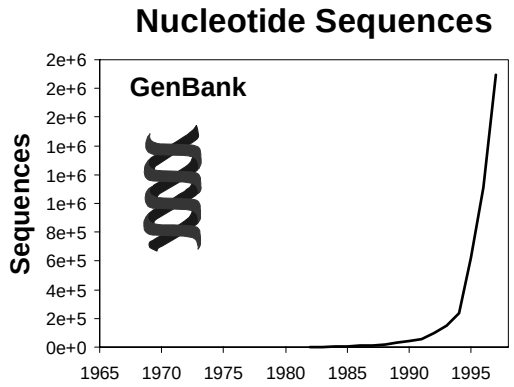
Nature 1997 Sep 18;389(6648):251-260

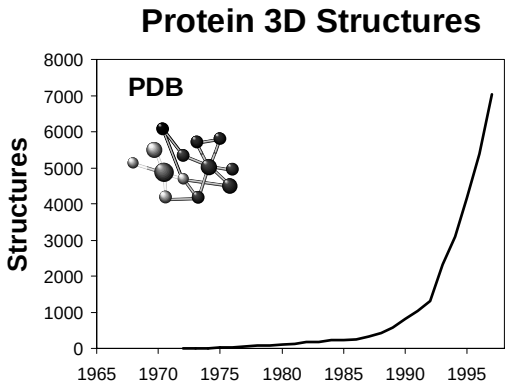
Crystal structure of the nucleosome core particle at 2.8 A resolution.

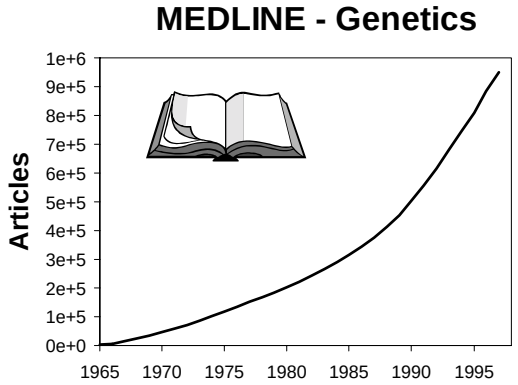
Luger K, Mader AW, Richmond RK, Sargent DF, Richmond TJ

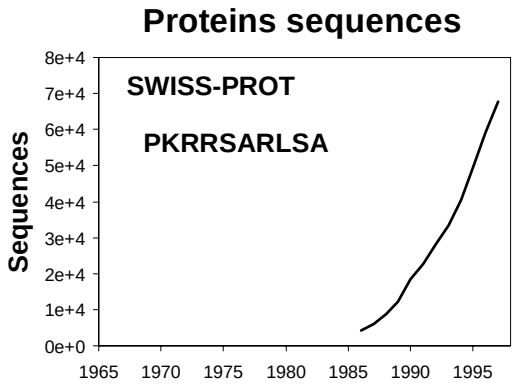
The Biotechnology Information Explosion

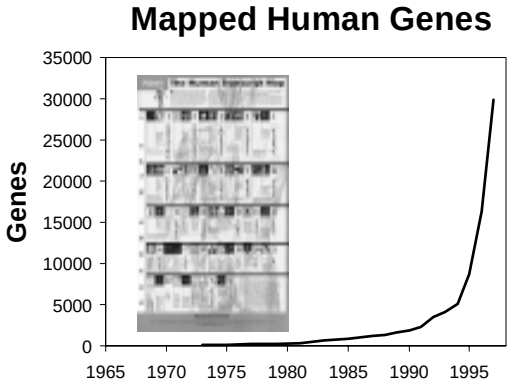




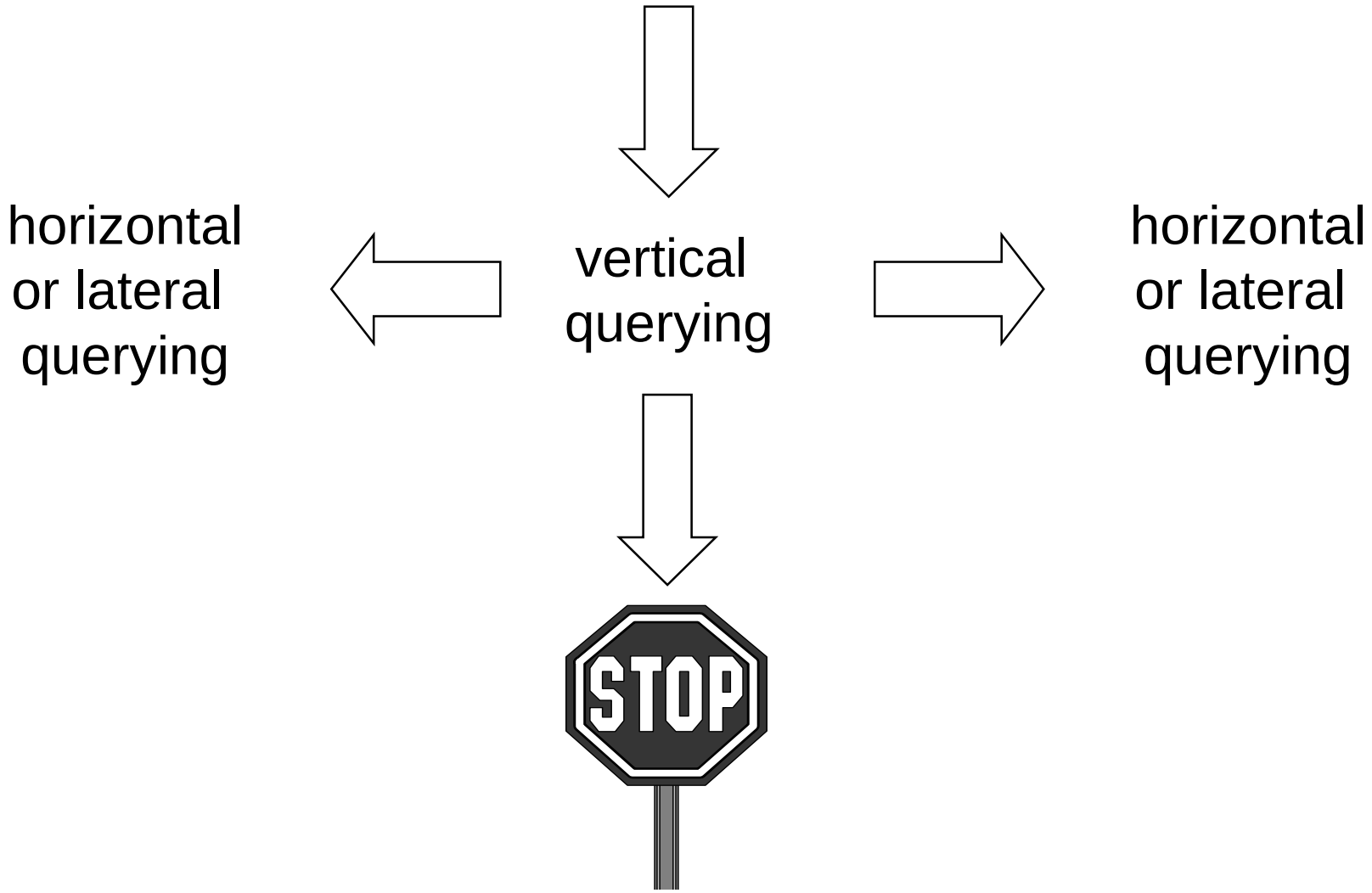




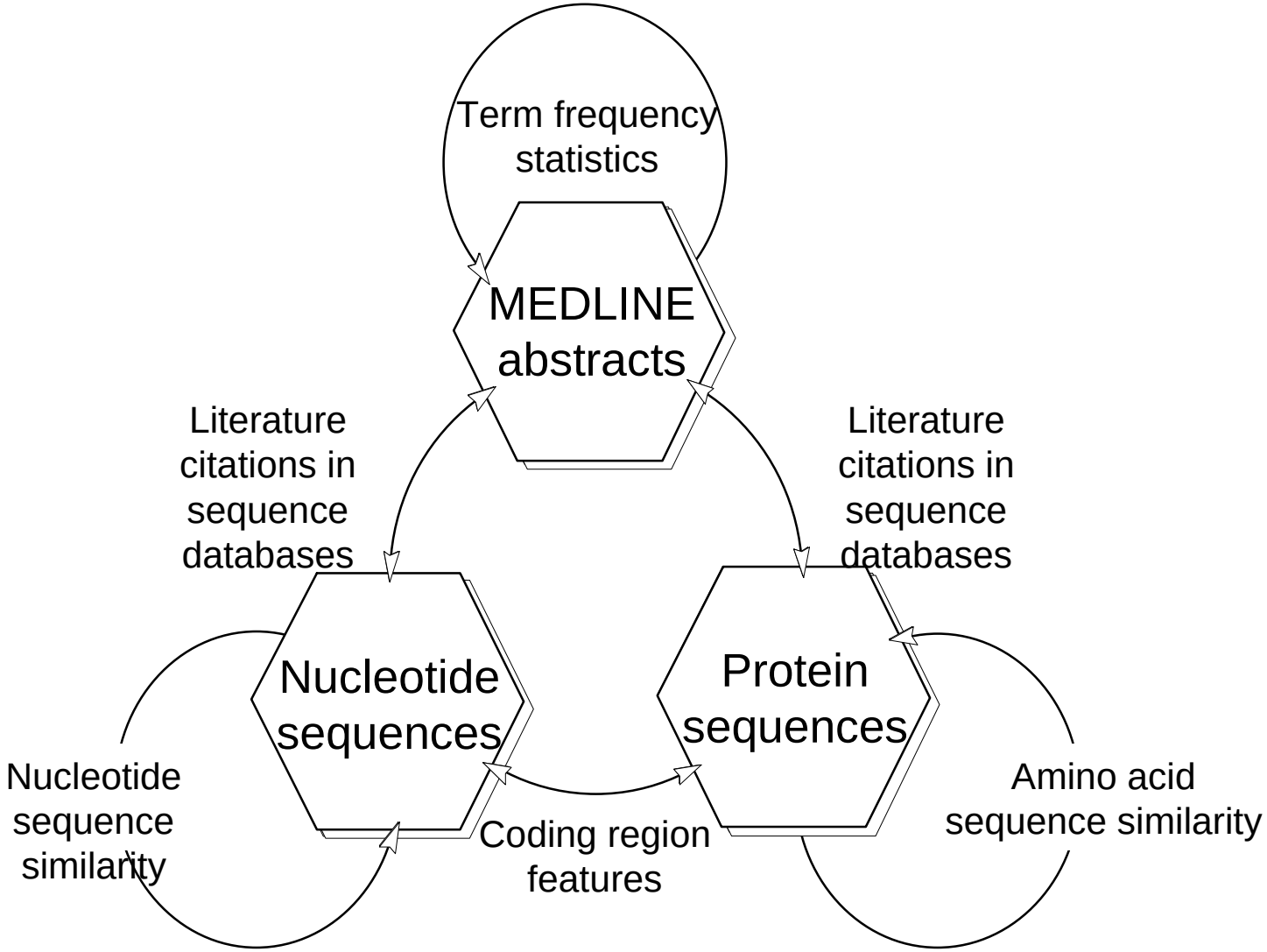




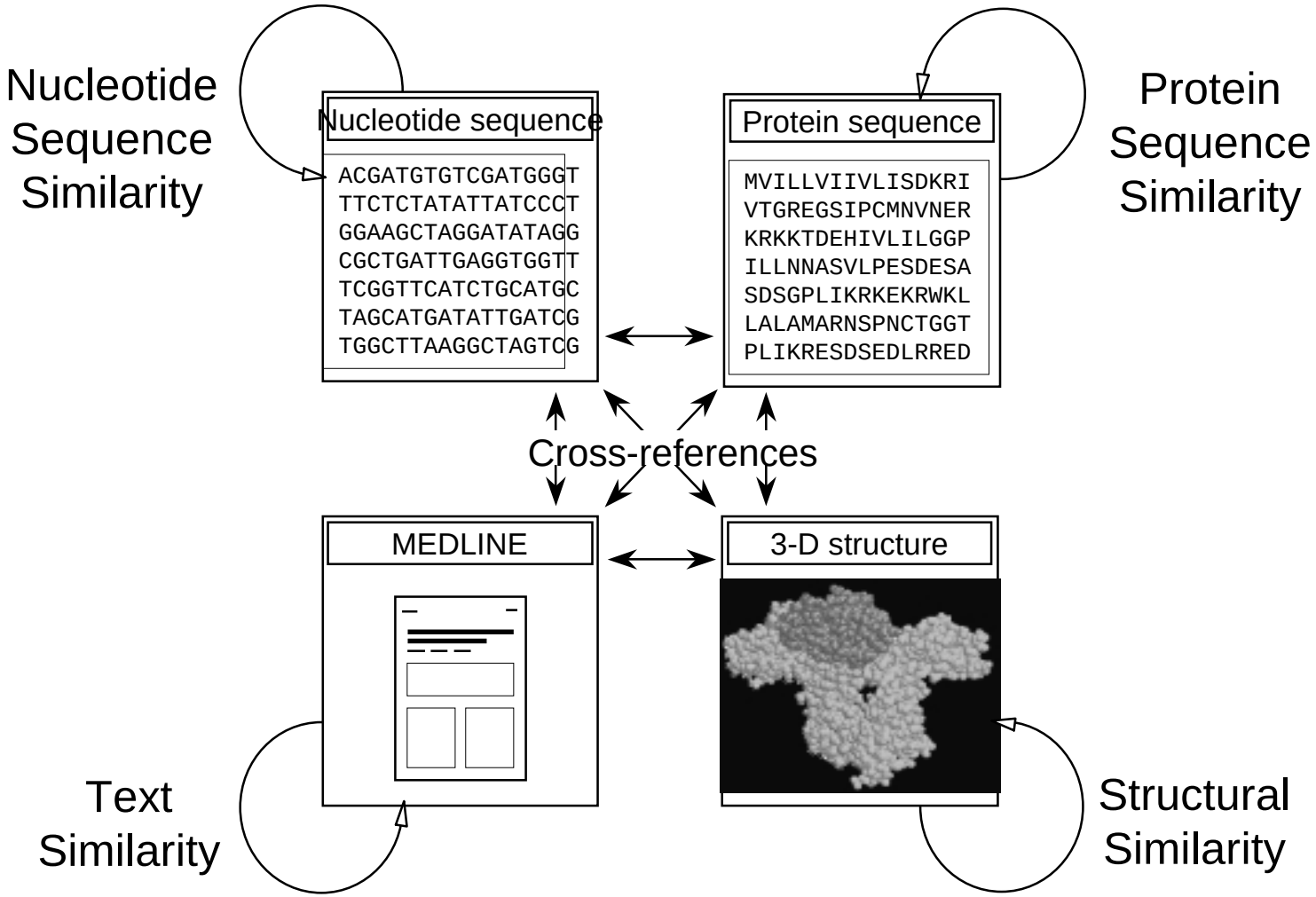
Entrez and its databases



Entrez (1992)


Term frequency statistics
MEDLINE abstracts
Literature citations in sequence databases
Literature citations in sequence databases
Nucleotide sequences
Protein sequences
Nucleotide sequence similarity
Coding region features
Amino acid sequence similarity

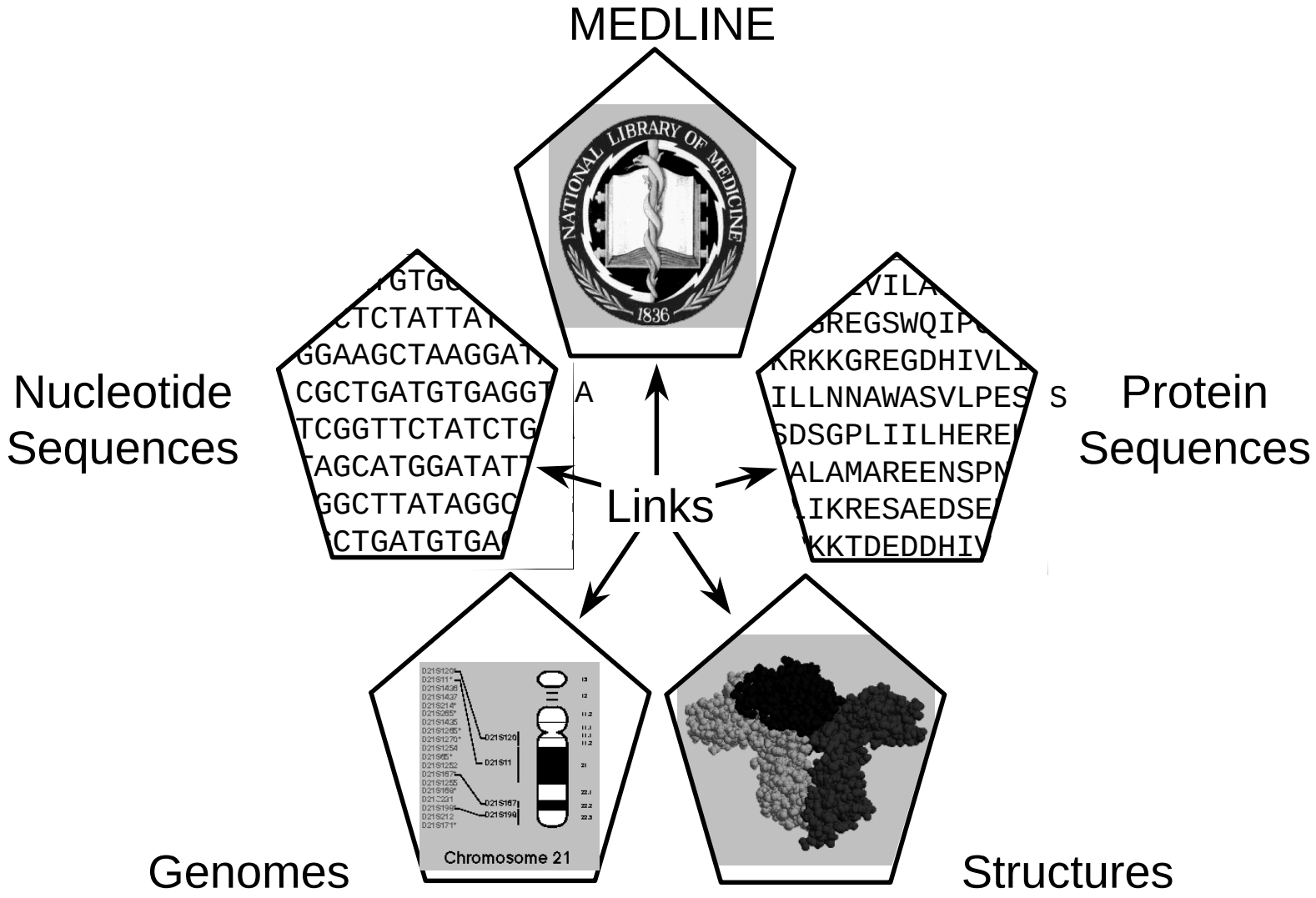
Entrez (1994)


Nucleotide Sequence Similarity
Nucleotide sequence
ACGATGTGTCGATGGGT
TTCTCTATATTATCCCT
GGAAGCTAGGATATAGG
CGCTGATTGAGGTGGTT
TCGGTTCATCTGCATGC
TAGCATGATATTGATCG
TGGCTTAAGGCTAGTCG
Protein sequence
MVILLVIIVLISDKRI
VTGREGSIPCMNVNER
KRKKTDEHIVLILGGP
ILLNNASVLPESDESA
SDSGPLIKRKEKRWKL
LALAMARNSPNCTGGT
PLIKRESDSEDLRRED
Protein Sequence Similarity
Cross-references
MEDLINE
3-D structure
Text Similarity
Structural Similarity

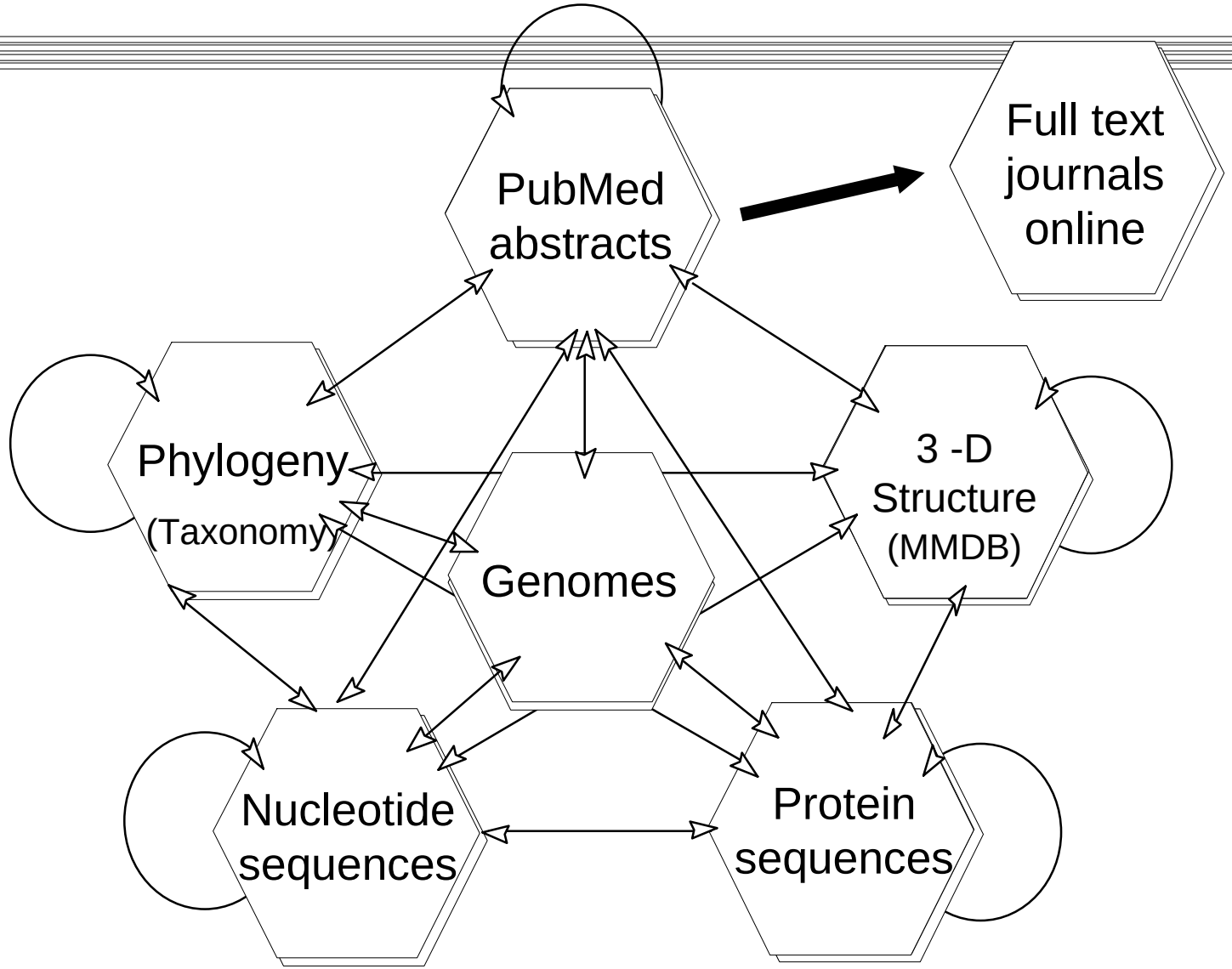
Entrez BigMed Data Set (Replaced by PubMed)

- Version 27.58; April 22, 1997
- 1,392,146 MEDLINE entries
  - All citations indexed under the MeSH term “Genetics” and its descendants (*i.e.* G5 tree)
  - Smaller subsets having to do with molecular sequences
  - Compare to total MEDLINE with ~ 8 million records
- 421,797 protein entries (“nr”)
- 1,273,697 nucleotide entries (“nr”)
- 4,873 structure entries (MMDB)
- 47,213 genome entries
- linked journals: *J. Biol. Chem., PNAS, Science, J.M.B.,* ++++

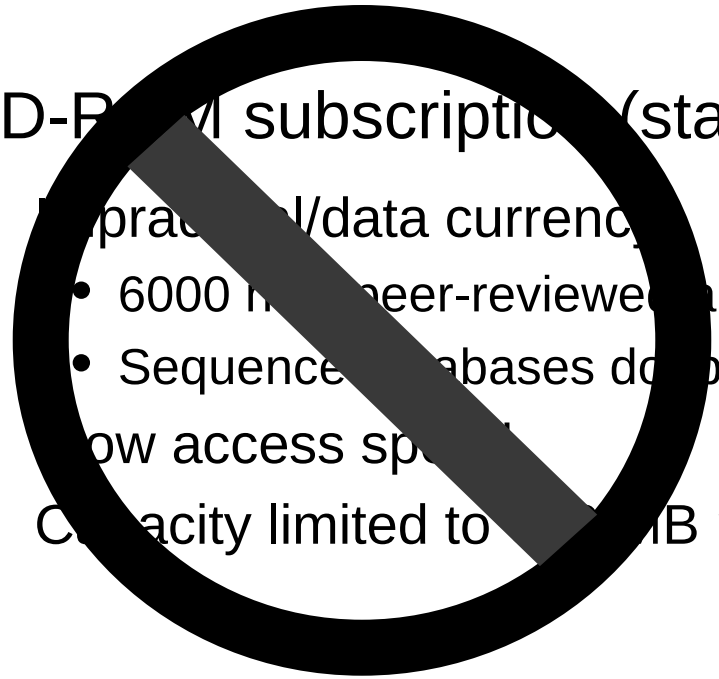
Entrez: Genotype to Phenotype (1996)



Entrez Increases Discovery Space 1998



Entrez Implementations



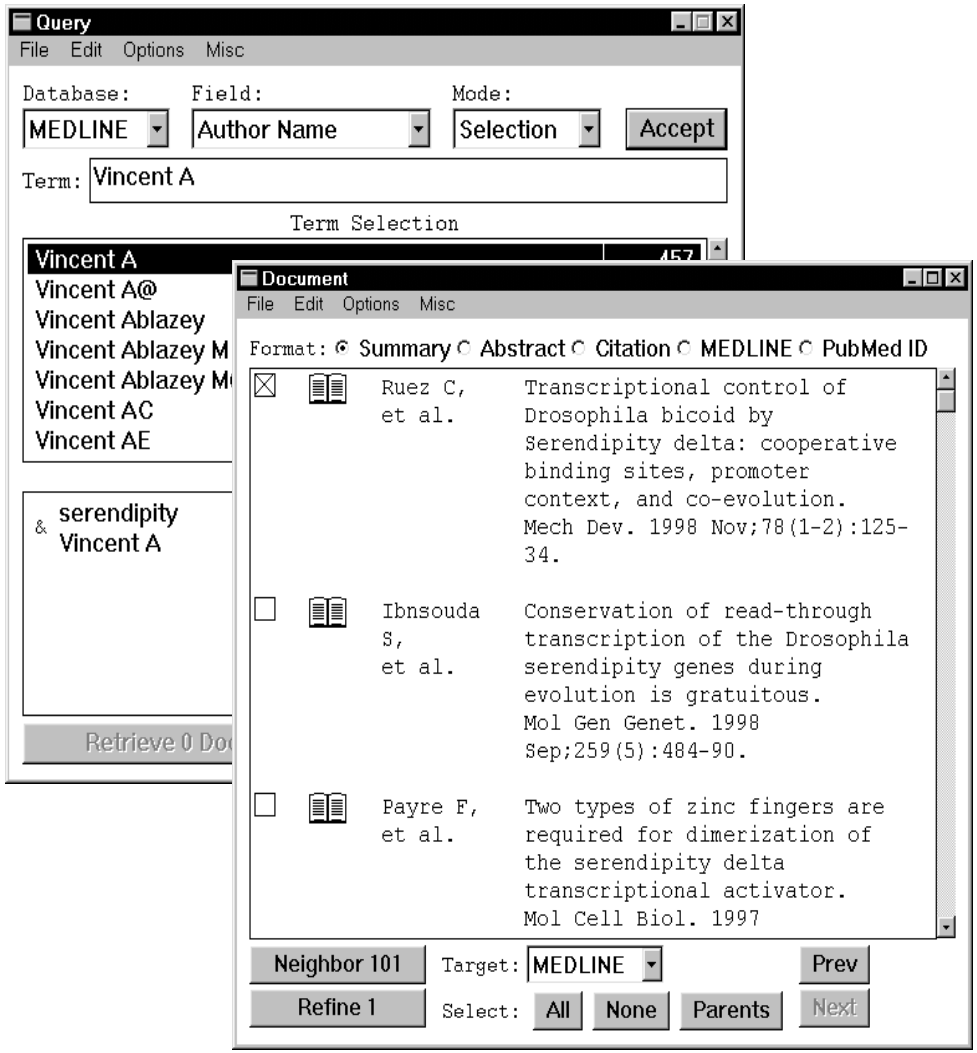
- CD-ROM subscriptions (stand-alone)
  - Impractical/data currency
    - 6000 new peer-reviewed articles per month
    - Sequence databases double ~20 months
  - Slow access speed
  - Capacity limited to 650 MB per CD-ROM

Entrez Implementations

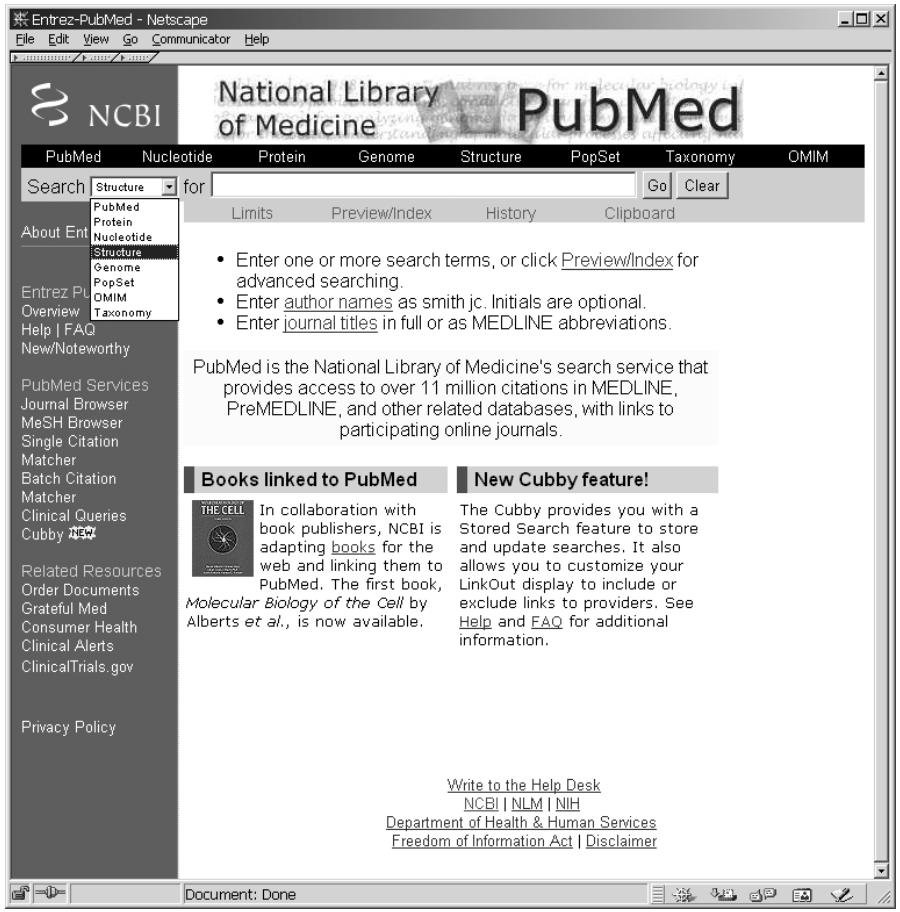
- **Network Entrez** (client-server)
  - Connect to dispatcher
  - Fastest Entrez implementation
  - Software installations and updates maintained by user
- **Web Entrez** (WWW client-server)
  - Universality of WWW
  - Can serve users without access to GUI environment (Lynx)
  - Linking and neighboring information can be expressed as hypertext
  - Ability to link to external data sources
  - WWW browsers are supported by third-party developers
  - Web implementation maintained by NCBI

Entrez Implementations

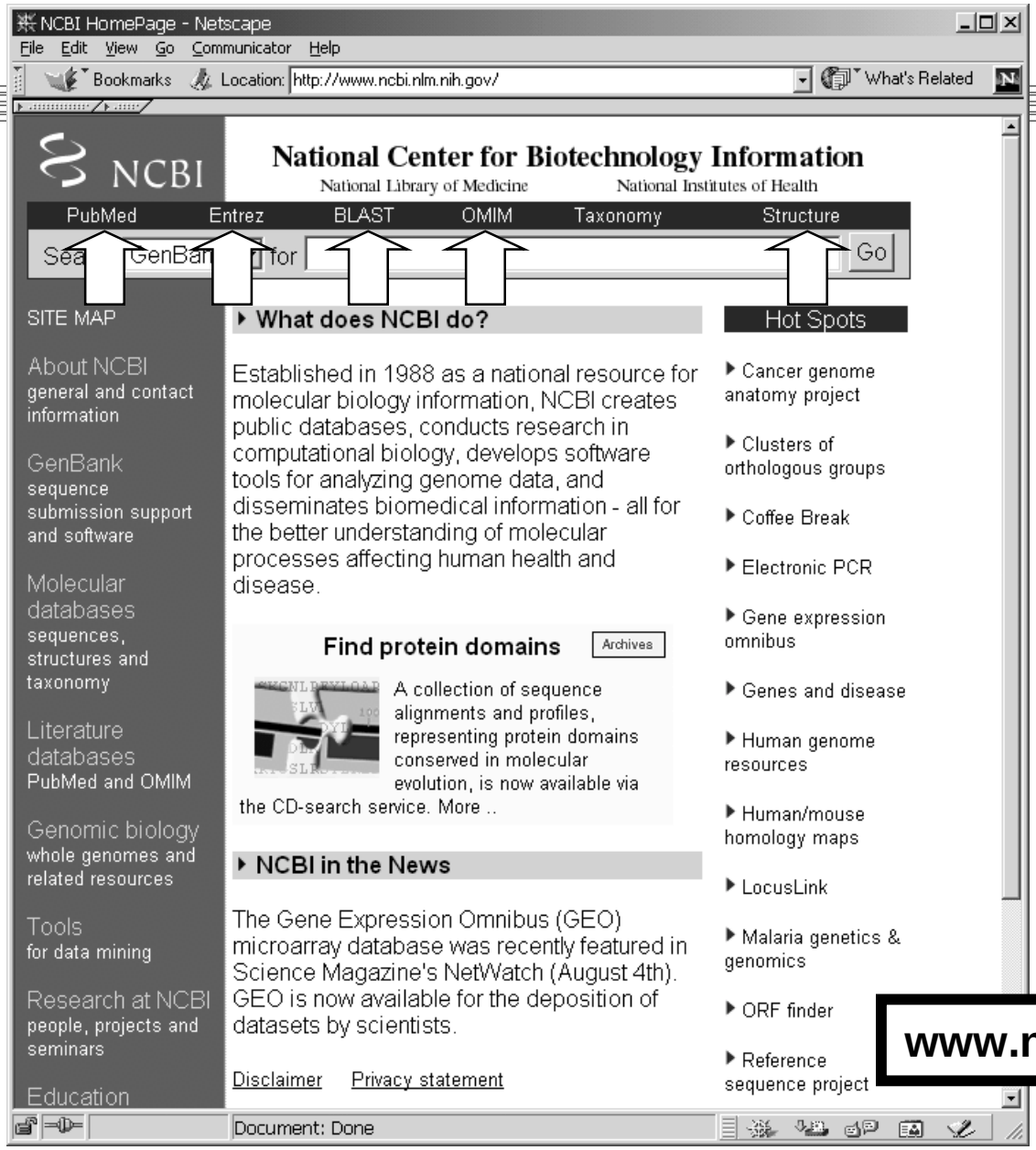
Network Entrez Version 6.6



Web Entrez



NCBI's Home Page

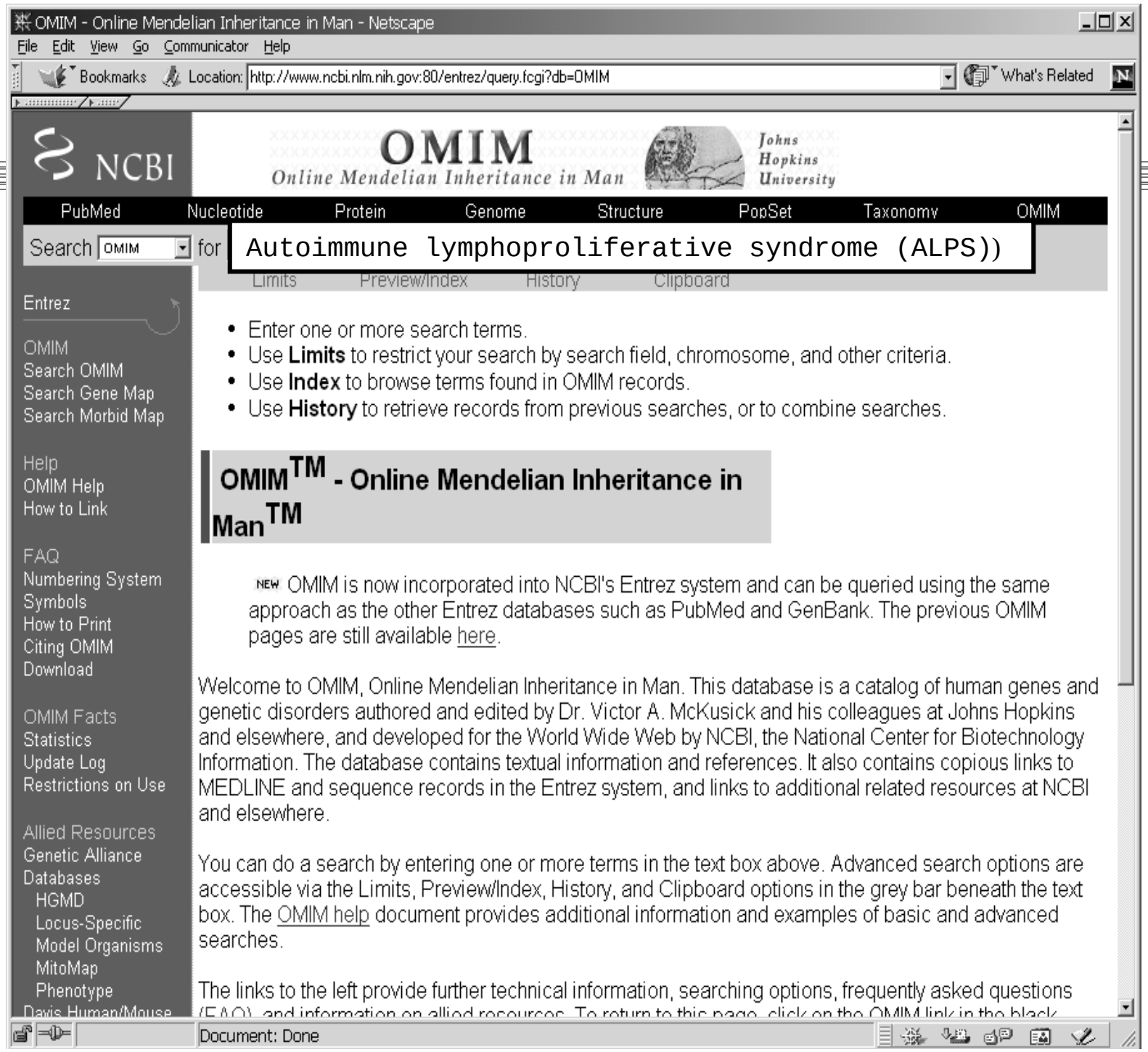


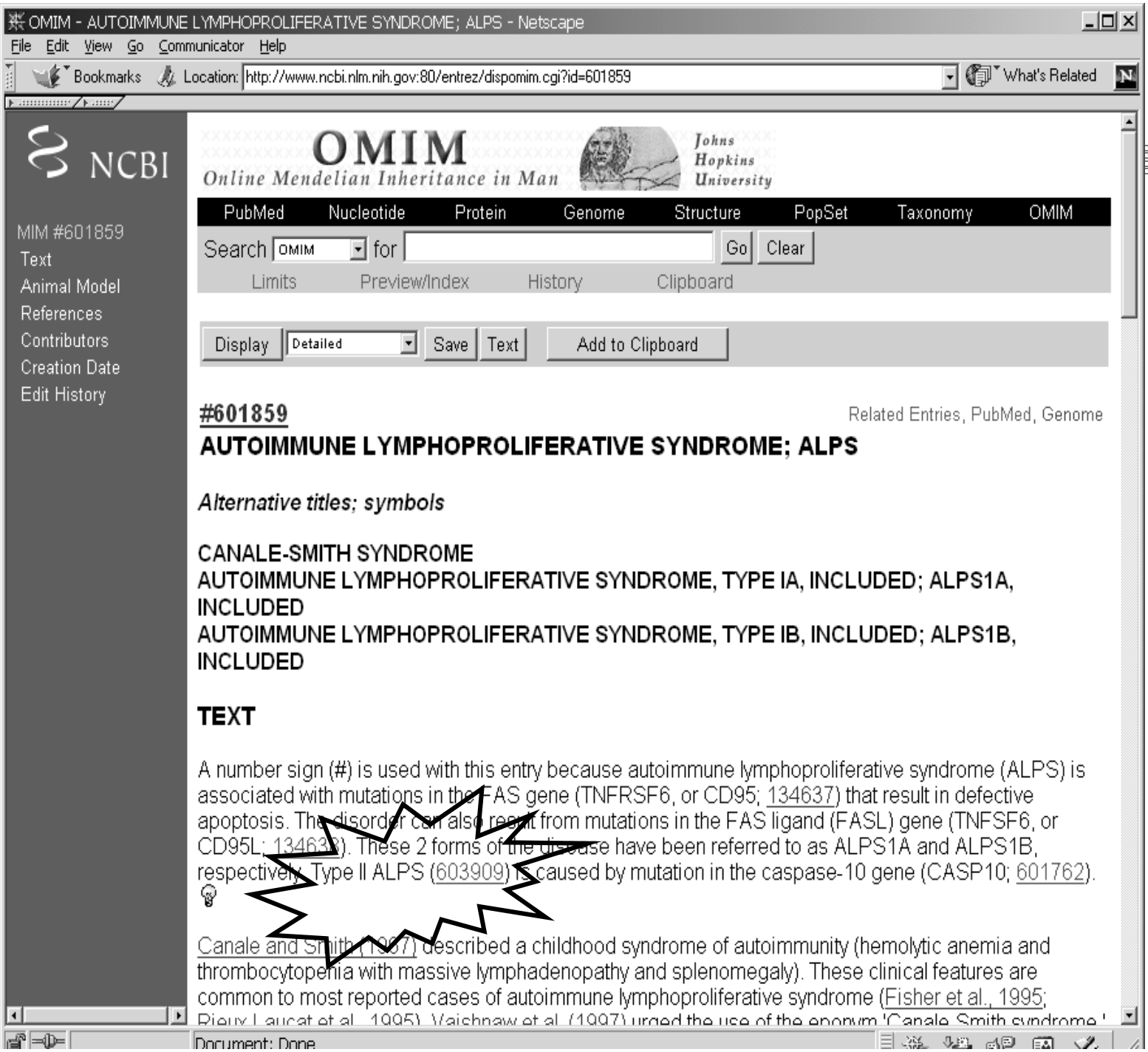
www.ncbi.nlm.nih.gov

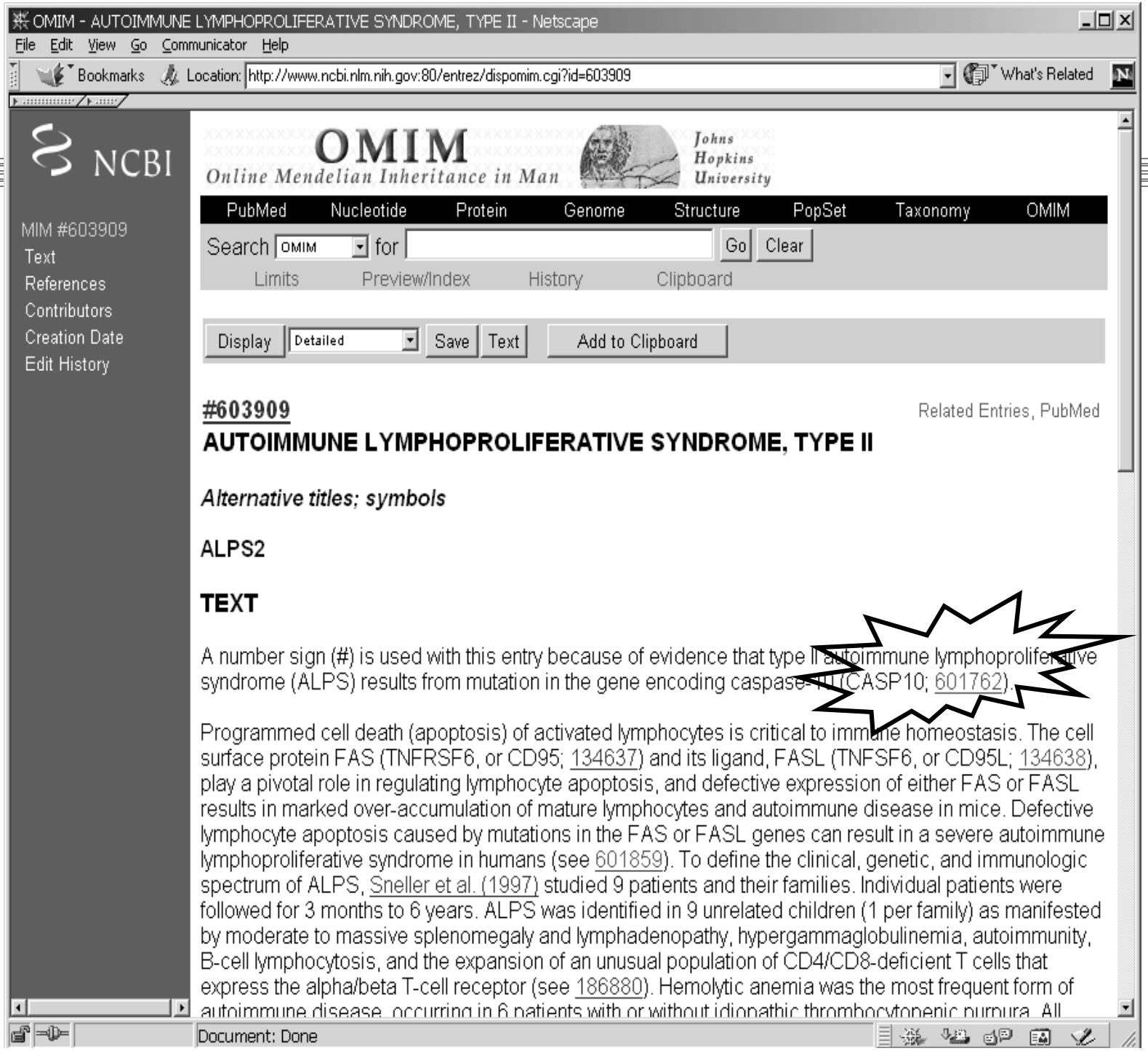
Objectives

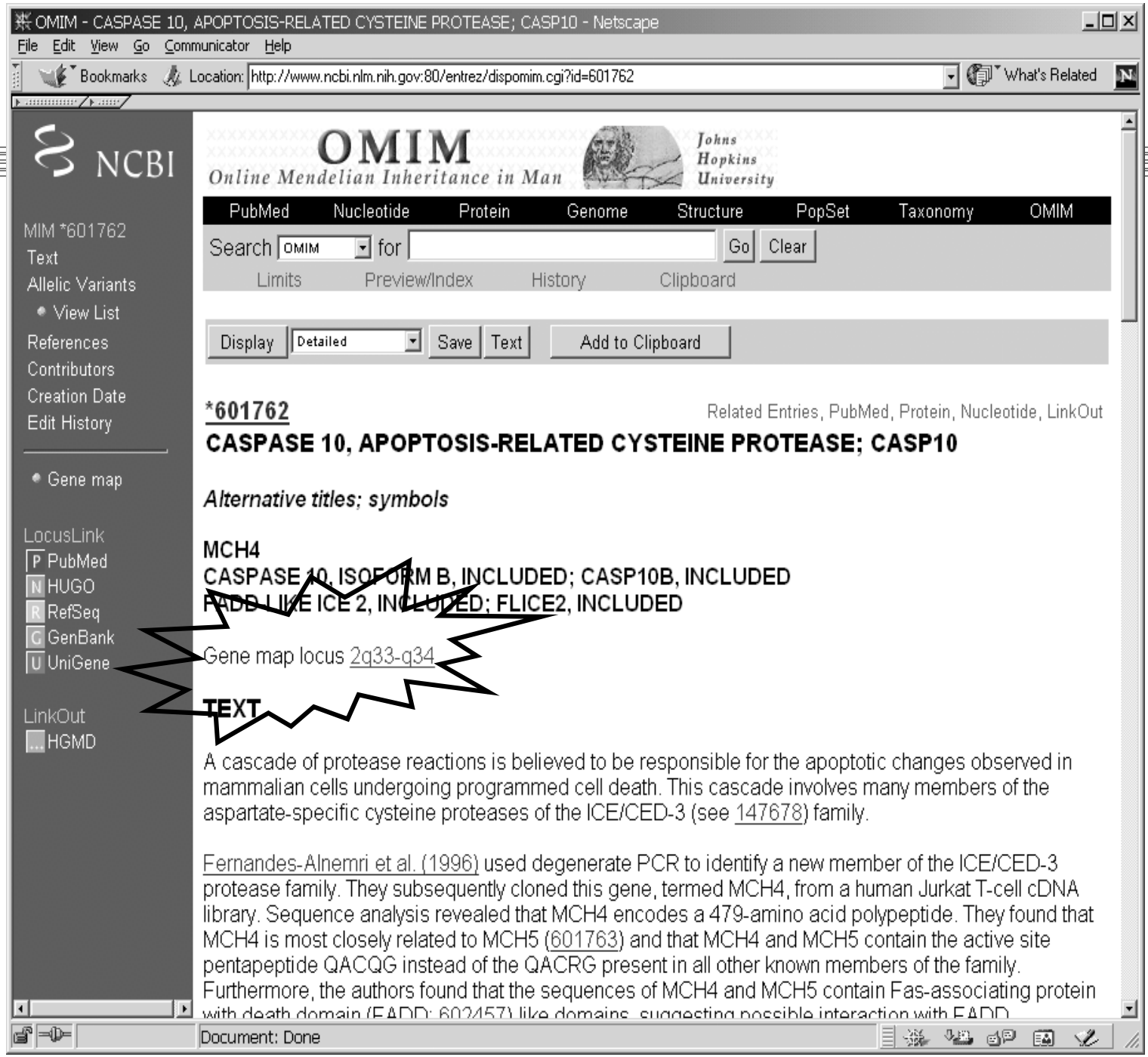
- start with a syndrome search in OMIM
- identify the gene for the syndrome
- locate the gene on the genome
    - other genes nearby
- information about the gene in LocusLink
- links to sequence and structure information
- view structurally similar proteins

- **The Cubby at the NCBI**


OMIM - Online Mendelian Inheritance in Man - Netscape
File Edit View Go Communicator Help
Bookmarks Location: http://www.ncbi.nlm.nih.gov:80/entrez/query.fcgi?db=OMIM
What's Related
NCBI
OMIM
Online Mendelian Inheritance in Man
Johns Hopkins University
PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM
Search OMIM for Autoimmune lymphoproliferative syndrome (ALPS))
Limits Preview/Index History Clipboard
Entrez
OMIM
Search OMIM
Search Gene Map
Search Morbid Map
Help
OMIM Help
How to Link
FAQ
Numbering System
Symbols
How to Print
Citing OMIM
Download
OMIM Facts
Statistics
Update Log
Restrictions on Use
Allied Resources
Genetic Alliance
Databases
HGMD
Locus-Specific
Model Organisms
MitoMap
Phenotype
Enter one or more search terms.
Use Limits to restrict your search by search field, chromosome, and other criteria.
Use Index to browse terms found in OMIM records.
Use History to retrieve records from previous searches, or to combine searches.
OMIM™ - Online Mendelian Inheritance in Man™
NEW OMIM is now incorporated into NCBI's Entrez system and can be queried using the same approach as the other Entrez databases such as PubMed and GenBank. The previous OMIM pages are still available here.
Welcome to OMIM, Online Mendelian Inheritance in Man. This database is a catalog of human genes and genetic disorders authored and edited by Dr. Victor A. McKusick and his colleagues at Johns Hopkins and elsewhere, and developed for the World Wide Web by NCBI, the National Center for Biotechnology Information. The database contains textual information and references. It also contains copious links to MEDLINE and sequence records in the Entrez system, and links to additional related resources at NCBI and elsewhere.
You can do a search by entering one or more terms in the text box above. Advanced search options are accessible via the Limits, Preview/Index, History, and Clipboard options in the grey bar beneath the text box. The OMIM help document provides additional information and examples of basic and advanced searches.
The links to the left provide further technical information, searching options, frequently asked questions
Document: Done


OMIM - AUTOIMMUNE LYMPHOPROLIFERATIVE SYNDROME; ALPS - Netscape
File Edit View Go Communicator Help
Bookmarks Location: http://www.ncbi.nlm.nih.gov:80/entrez/dispomim.cgi?id=601859
What's Related
NCBI
OMIM
Online Mendelian Inheritance in Man
Johns Hopkins University
PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM
Search OMIM for Go Clear
Limits Preview/Index History Clipboard
MIM #601859
Text
Animal Model
References
Contributors
Creation Date
Edit History
Display Detailed Save Text Add to Clipboard
#601859
Related Entries, PubMed, Genome
AUTOIMMUNE LYMPHOPROLIFERATIVE SYNDROME; ALPS
Alternative titles; symbols
CANALE-SMITH SYNDROME
AUTOIMMUNE LYMPHOPROLIFERATIVE SYNDROME, TYPE IA, INCLUDED; ALPS1A, INCLUDED
AUTOIMMUNE LYMPHOPROLIFERATIVE SYNDROME, TYPE IB, INCLUDED; ALPS1B, INCLUDED
TEXT
A number sign (#) is used with this entry because autoimmune lymphoproliferative syndrome (ALPS) is associated with mutations in the FAS gene (TNFRSF6, or CD95; 134637) that result in defective apoptosis. The disorder can also result from mutations in the FAS ligand (FASL) gene (TNFSF6, or CD95L; 134638). These 2 forms of the disease have been referred to as ALPS1A and ALPS1B, respectively. Type II ALPS (603909) is caused by mutation in the caspase-10 gene (CASP10; 601762).
Canale and Smith (1967) described a childhood syndrome of autoimmunity (hemolytic anemia and thrombocytopenia with massive lymphadenopathy and splenomegaly). These clinical features are common to most reported cases of autoimmune lymphoproliferative syndrome (Fisher et al., 1995;
Document: Done


OMIM - AUTOIMMUNE LYMPHOPROLIFERATIVE SYNDROME, TYPE II - Netscape
File Edit View Go Communicator Help
Bookmarks Location: http://www.ncbi.nlm.nih.gov:80/entrez/dispomim.cgi?id=603909 What's Related
NCBI
OMIM
Online Mendelian Inheritance in Man
Johns Hopkins University
PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM
Search OMIM for Go Clear
Limits Preview/Index History Clipboard
MIM #603909
Text
References
Contributors
Creation Date
Edit History
Display Detailed Save Text Add to Clipboard
#603909
Related Entries, PubMed
AUTOIMMUNE LYMPHOPROLIFERATIVE SYNDROME, TYPE II
Alternative titles; symbols
ALPS2
TEXT
A number sign (#) is used with this entry because of evidence that type II autoimmune lymphoproliferative syndrome (ALPS) results from mutation in the gene encoding caspase-10 (CASP10; 601762).
Programmed cell death (apoptosis) of activated lymphocytes is critical to immune homeostasis. The cell surface protein FAS (TNFRSF6, or CD95; 134637) and its ligand, FASL (TNFSF6, or CD95L; 134638), play a pivotal role in regulating lymphocyte apoptosis, and defective expression of either FAS or FASL results in marked over-accumulation of mature lymphocytes and autoimmune disease in mice. Defective lymphocyte apoptosis caused by mutations in the FAS or FASL genes can result in a severe autoimmune lymphoproliferative syndrome in humans (see 601859). To define the clinical, genetic, and immunologic spectrum of ALPS, Sneller et al. (1997) studied 9 patients and their families. Individual patients were followed for 3 months to 6 years. ALPS was identified in 9 unrelated children (1 per family) as manifested by moderate to massive splenomegaly and lymphadenopathy, hypergammaglobulinemia, autoimmunity, B-cell lymphocytosis, and the expansion of an unusual population of CD4/CD8-deficient T cells that express the alpha/beta T-cell receptor (see 186880). Hemolytic anemia was the most frequent form of autoimmune disease, occurring in 6 patients with or without idiopathic thrombocytopenic purpura. All
Document: Done


OMIM - CASPASE 10, APOPTOSIS-RELATED CYSTEINE PROTEASE; CASP10 - Netscape
File Edit View Go Communicator Help
Bookmarks Location: http://www.ncbi.nlm.nih.gov:80/entrez/dispomim.cgi?id=601762
What's Related
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Johns Hopkins University
PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM
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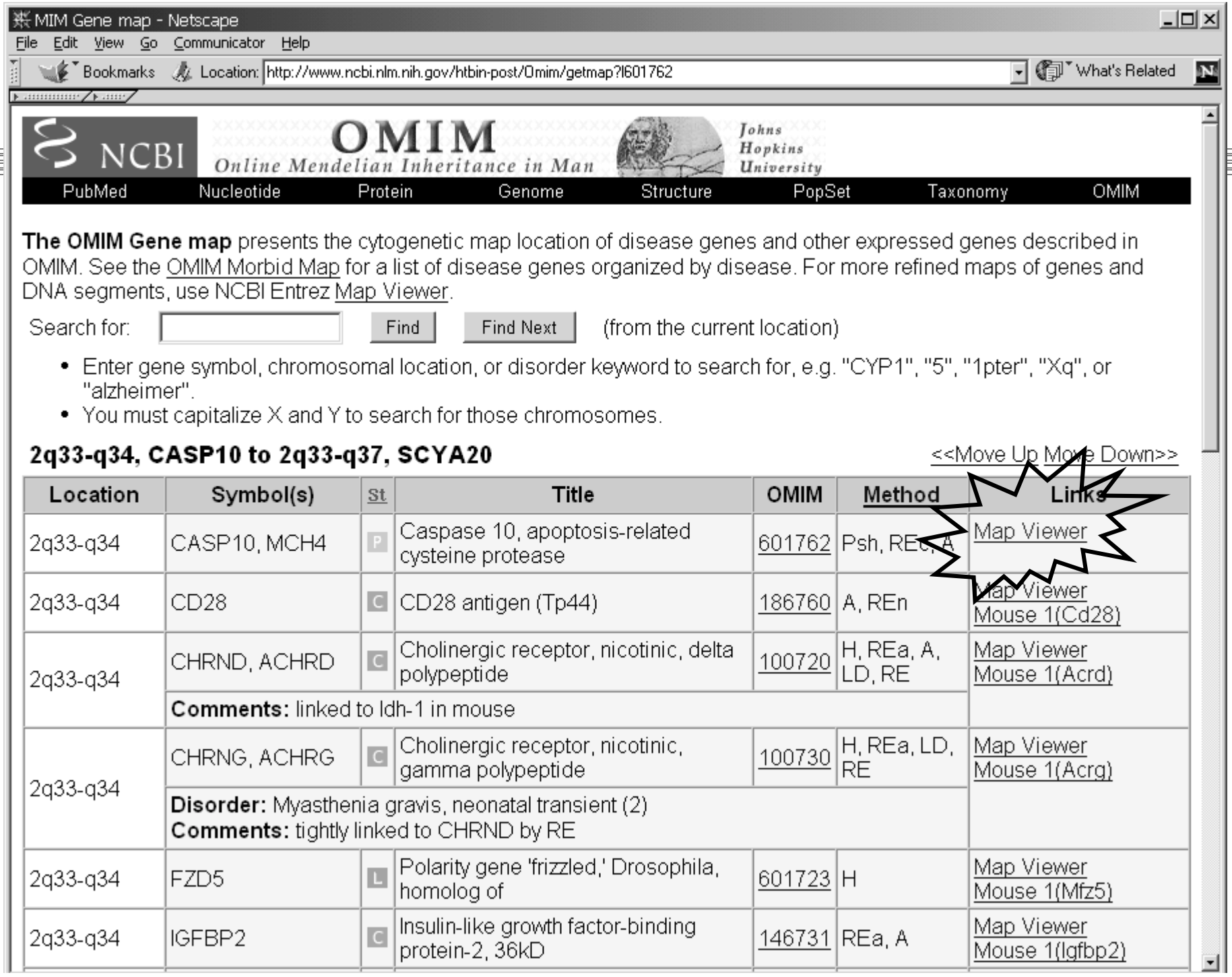
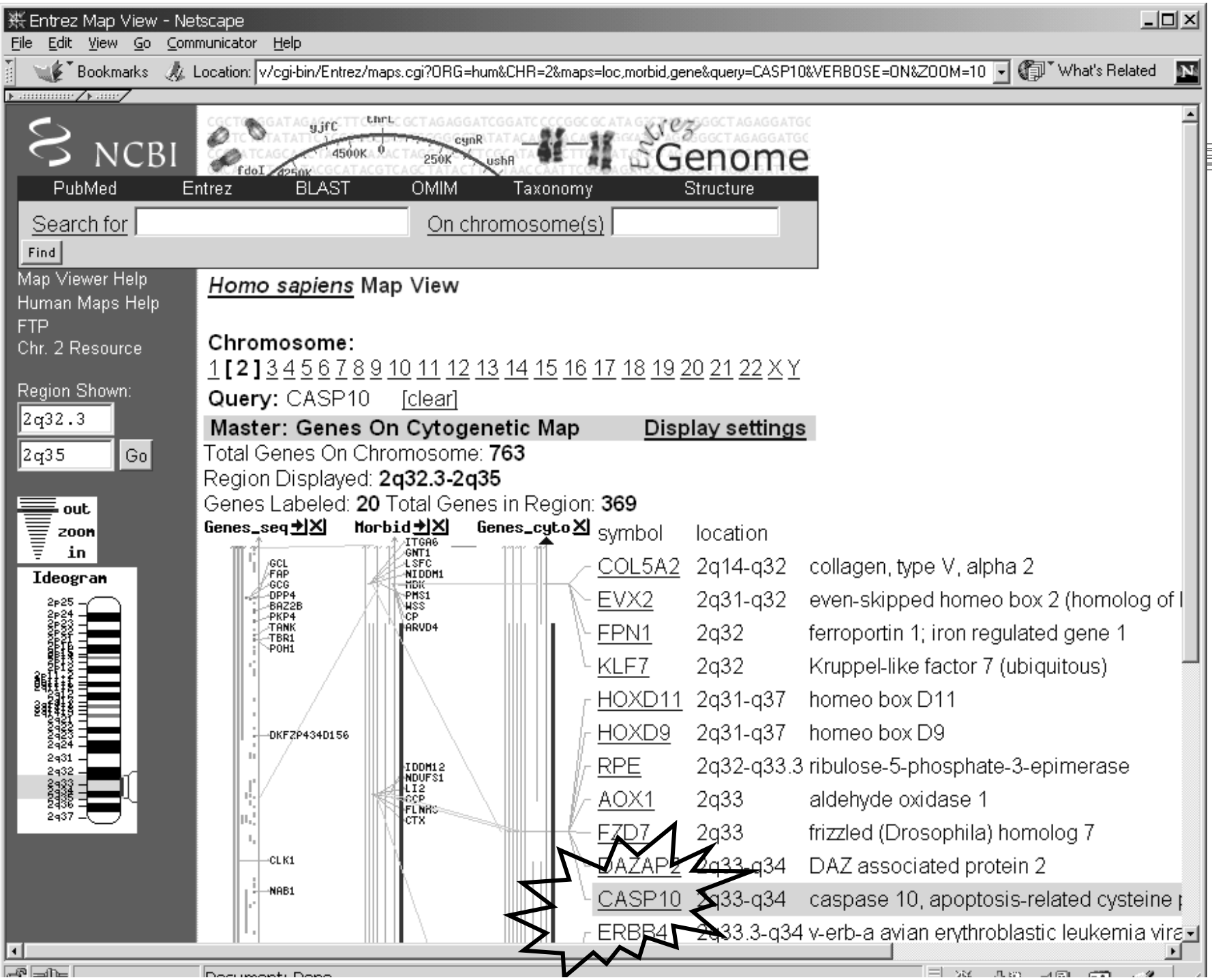
Limits Preview/Index History Clipboard
Display Detailed Save Text Add to Clipboard
MIM *601762
Text
Allelic Variants
View List
References
Contributors
Creation Date
Edit History
Gene map
LocusLink
PubMed
HUGO
RefSeq
GenBank
UniGene
LinkOut
HGMD
*601762
Related Entries, PubMed, Protein, Nucleotide, LinkOut
CASPASE 10, APOPTOSIS-RELATED CYSTEINE PROTEASE; CASP10
Alternative titles; symbols
MCH4
CASPASE 10, ISOFORM B, INCLUDED; CASP10B, INCLUDED
FADD-LIKE ICE 2, INCLUDED; FLICE2, INCLUDED
Gene map locus 2q33-q34
TEXT
A cascade of protease reactions is believed to be responsible for the apoptotic changes observed in mammalian cells undergoing programmed cell death. This cascade involves many members of the aspartate-specific cysteine proteases of the ICE/CED-3 (see 147678) family.
Fernandes-Alnemri et al. (1996) used degenerate PCR to identify a new member of the ICE/CED-3 protease family. They subsequently cloned this gene, termed MCH4, from a human Jurkat T-cell cDNA library. Sequence analysis revealed that MCH4 encodes a 479-amino acid polypeptide. They found that MCH4 is most closely related to MCH5 (601763) and that MCH4 and MCH5 contain the active site pentapeptide QACQG instead of the QACRG present in all other known members of the family. Furthermore, the authors found that the sequences of MCH4 and MCH5 contain Fas-associating protein
Document: Done


MIM Gene map - Netscape
File Edit View Go Communicator Help
Bookmarks Location: http://www.ncbi.nlm.nih.gov/htbin-post/Omim/getmap?l601762
What's Related
NCBI
OMIM
Online Mendelian Inheritance in Man
Johns Hopkins University
PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM
The OMIM Gene map presents the cytogenetic map location of disease genes and other expressed genes described in OMIM. See the OMIM Morbid Map for a list of disease genes organized by disease. For more refined maps of genes and DNA segments, use NCBI Entrez Map Viewer.
Search for:
Find
Find Next
(from the current location)
Enter gene symbol, chromosomal location, or disorder keyword to search for, e.g. "CYP1", "5", "1pter", "Xq", or "alzheimer".
You must capitalize X and Y to search for those chromosomes.
2q33-q34, CASP10 to 2q33-q37, SCYA20
<<Move Up Move Down>>
Location
Symbol(s)
St
Title
OMIM
Method
Links
2q33-q34
CASP10, MCH4
P
Caspase 10, apoptosis-related cysteine protease
601762
Psh, REc, A
Map Viewer
2q33-q34
CD28
C
CD28 antigen (Tp44)
186760
A, REn
Map Viewer
Mouse 1(Cd28)
2q33-q34
CHRND, ACHRD
C
Cholinergic receptor, nicotinic, delta polypeptide
100720
H, REa, A, LD, RE
Map Viewer
Mouse 1(Acrd)
Comments: linked to ldh-1 in mouse
2q33-q34
CHRNG, ACHRG
C
Cholinergic receptor, nicotinic, gamma polypeptide
100730
H, REa, LD, RE
Map Viewer
Mouse 1(Acrg)
Disorder: Myasthenia gravis, neonatal transient (2)
Comments: tightly linked to CHRND by RE
2q33-q34
FZD5
L
Polarity gene 'frizzled,' Drosophila, homolog of
601723
H
Map Viewer
Mouse 1(Mfz5)
2q33-q34
IGFBP2
C
Insulin-like growth factor-binding protein-2, 36kD
146731
REa, A
Map Viewer
Mouse 1(Igfbp2)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Region Shown:
2q32.3
2q35
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Ideogram
Homo sapiens Map View
Chromosome:
1 [2] 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
Query: CASP10 [clear]
Master: Genes On Cytogenetic Map
Display settings
Total Genes On Chromosome: 763
Region Displayed: 2q32.3-2q35
Genes Labeled: 20 Total Genes in Region: 369
Genes_seq
Morbid
Genes_cyto
symbol location
COL5A2 2q14-q32 collagen, type V, alpha 2
EVX2 2q31-q32 even-skipped homeo box 2 (homolog of
FPN1 2q32 ferroportin 1; iron regulated gene 1
KLF7 2q32 Kruppel-like factor 7 (ubiquitous)
HOXD11 2q31-q37 homeo box D11
HOXD9 2q31-q37 homeo box D9
RPE 2q32-q33.3 ribulose-5-phosphate-3-epimerase
AOX1 2q33 aldehyde oxidase 1
FZD7 2q33 frizzled (Drosophila) homolog 7
DAZAP2 2q33-q34 DAZ associated protein 2
CASP10 2q33-q34 caspase 10, apoptosis-related cysteine
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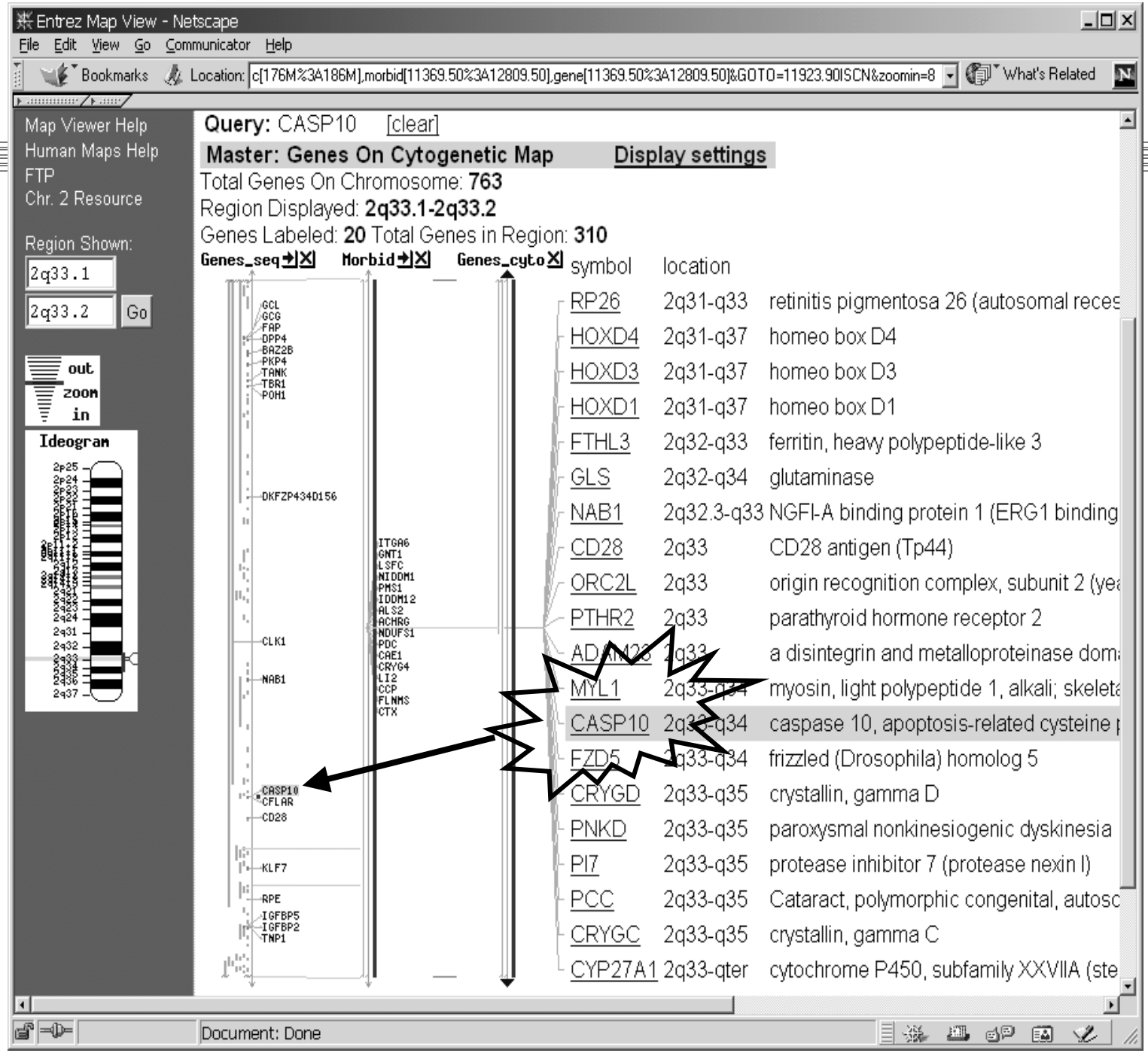
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2q33.2
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in
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Genes Labeled: 20 Total Genes in Region: 310
Genes_seq
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Genes_cyto
symbol location
RP26 2q31-q33 retinitis pigmentosa 26 (autosomal reces
HOXD4 2q31-q37 homeo box D4
HOXD3 2q31-q37 homeo box D3
HOXD1 2q31-q37 homeo box D1
FTHL3 2q32-q33 ferritin, heavy polypeptide-like 3
GLS 2q32-q34 glutaminase
NAB1 2q32.3-q33 NGFI-A binding protein 1 (ERG1 binding
CD28 2q33 CD28 antigen (Tp44)
ORC2L 2q33 origin recognition complex, subunit 2 (yea
PTHR2 2q33 parathyroid hormone receptor 2
MYL1 myosin, light polypeptide 1, alkali; skeleta
CASP10 caspase 10, apoptosis-related cysteine p
FZD5 frizzled (Drosophila) homolog 5
CRYGD 2q33-q35 crystallin, gamma D
PNKD 2q33-q35 paroxysmal nonkinesiogenic dyskinesia
PI7 2q33-q35 protease inhibitor 7 (protease nexin I)
PCC 2q33-q35 Cataract, polymorphic congenital, autosc
CRYGC 2q33-q35 crystallin, gamma C
CYP27A1 2q33-qter cytochrome P450, subfamily XXVIIA (ste
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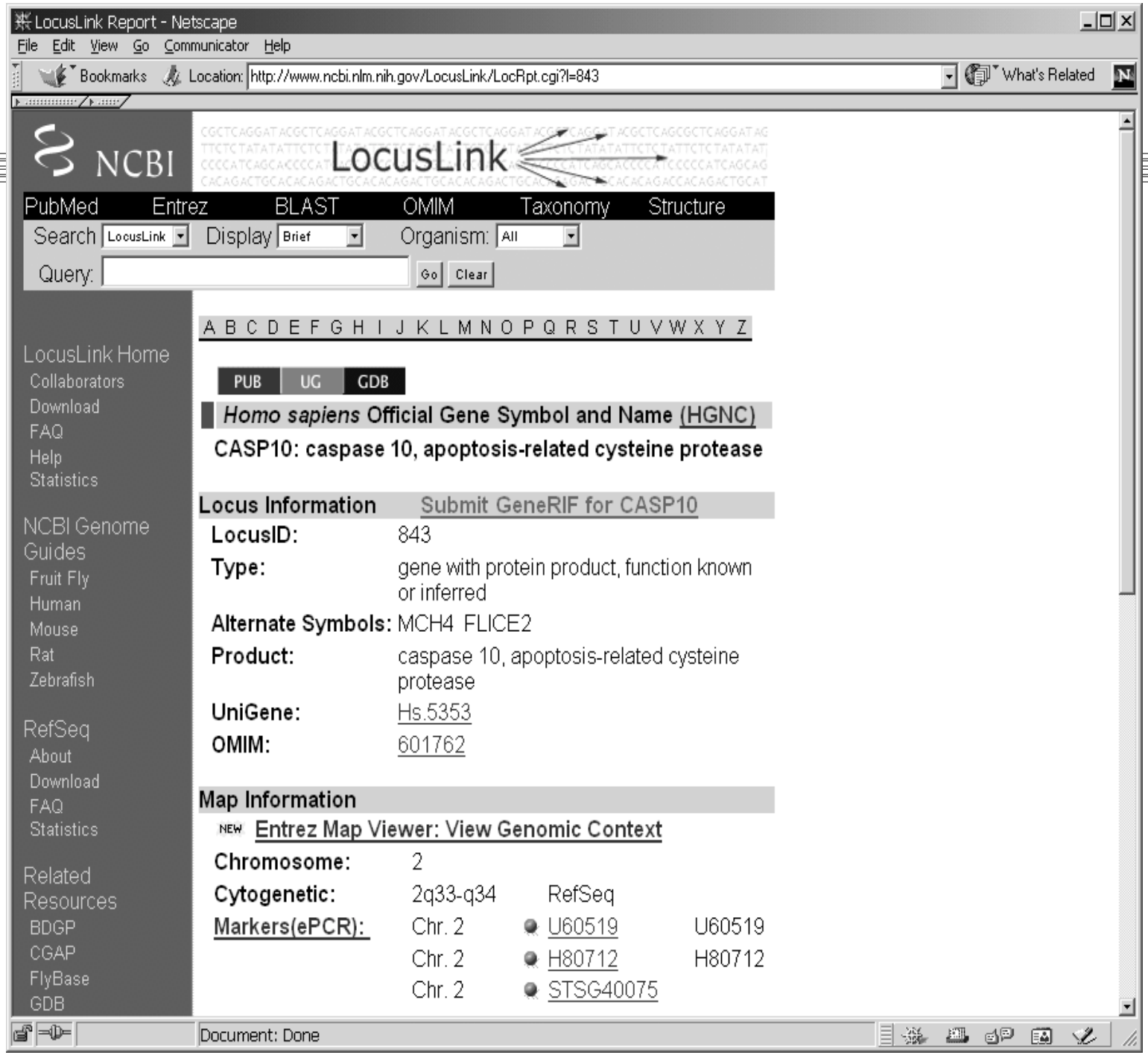
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CASP10: caspase 10, apoptosis-related cysteine protease
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Submit GeneRIF for CASP10
LocusID: 843
Type: gene with protein product, function known or inferred
Alternate Symbols: MCH4 FLICE2
Product: caspase 10, apoptosis-related cysteine protease
UniGene: Hs.5353
OMIM: 601762
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Chr. 2 STSG40075
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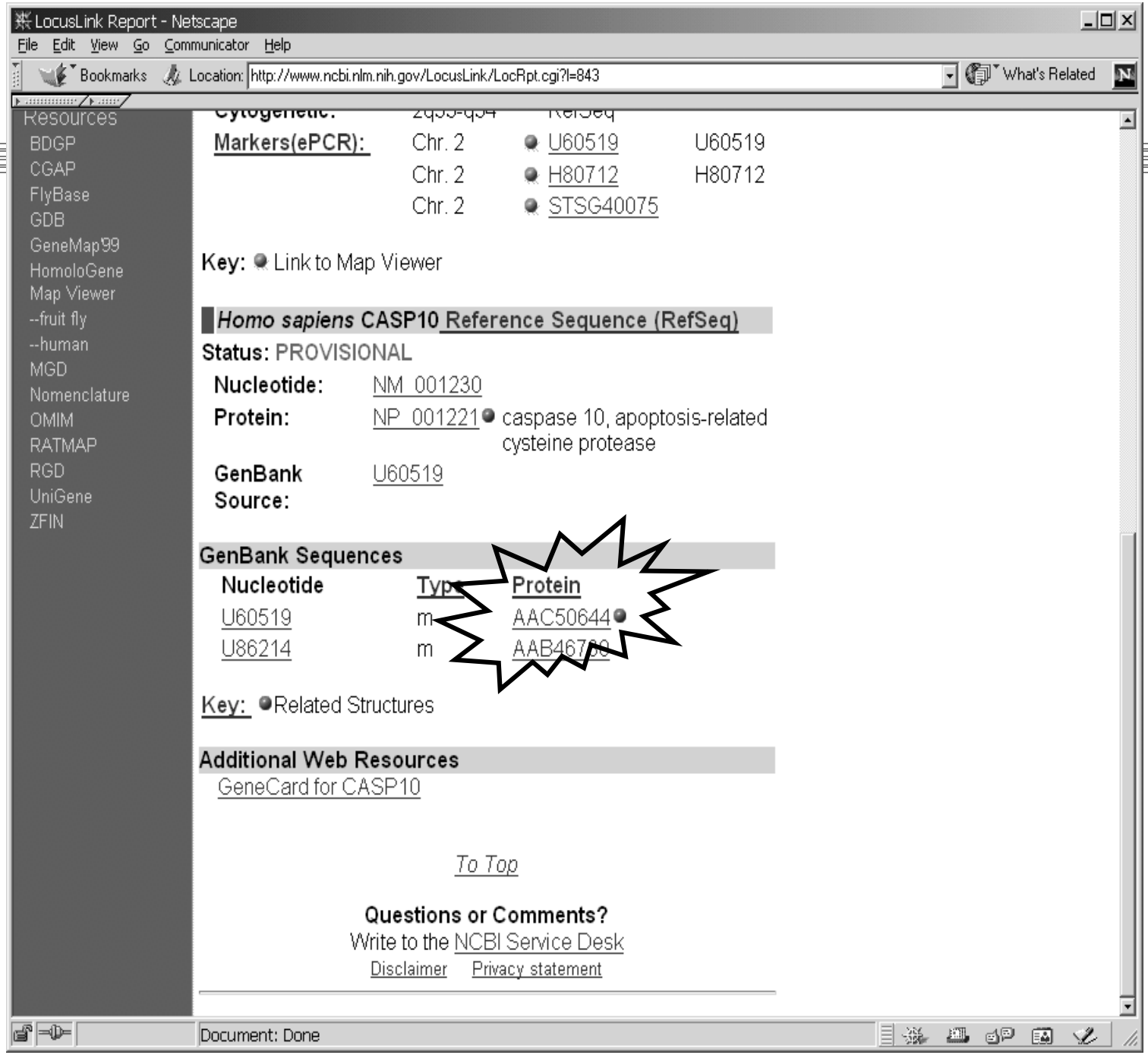
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Nucleotide: NM_001230
Protein: NP_001221 caspase 10, apoptosis-related cysteine protease
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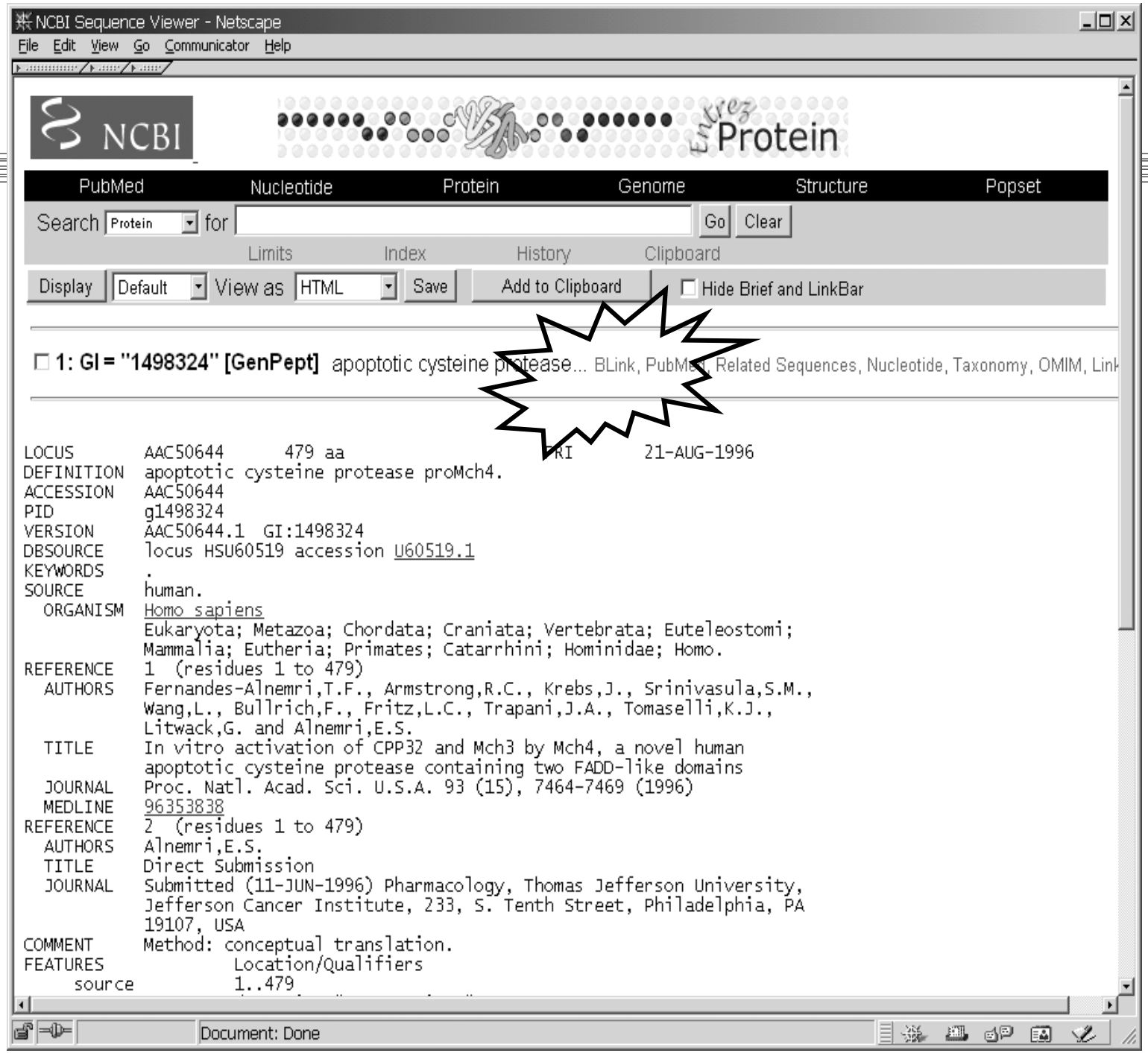
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DEFINITION apoptotic cysteine protease proMch4.
ACCESSION AAC50644
PID g1498324
VERSION AAC50644.1 GI:1498324
DBSOURCE locus HSU60519 accession U60519.1
KEYWORDS .
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (residues 1 to 479)
AUTHORS Fernandes-Alnemri,T.F., Armstrong,R.C., Krebs,J., Srinivasula,S.M.,
Wang,L., Bullrich,F., Fritz,L.C., Trapani,J.A., Tomaselli,K.J.,
Litwack,G. and Alnemri,E.S.
TITLE In vitro activation of CPP32 and Mch3 by Mch4, a novel human
apoptotic cysteine protease containing two FADD-like domains
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (15), 7464-7469 (1996)
MEDLINE 96353838
REFERENCE 2 (residues 1 to 479)
AUTHORS Alnemri,E.S.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-1996) Pharmacology, Thomas Jefferson University,
Jefferson Cancer Institute, 233, S. Tenth Street, Philadelphia, PA
19107, USA
COMMENT Method: conceptual translation.
FEATURES Location/Qualifiers
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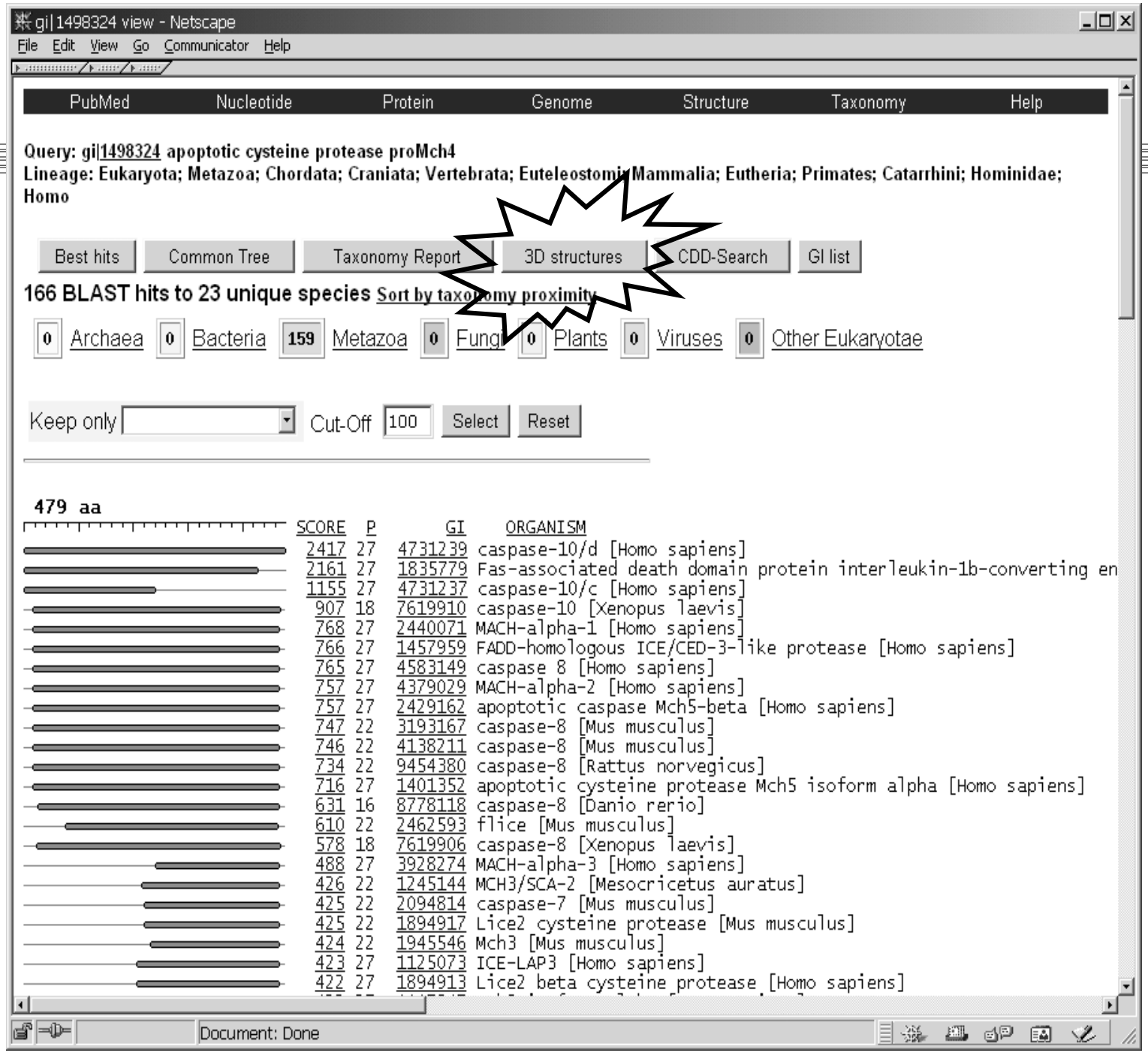
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0 Bacteria
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0 Viruses
0 Other Eukaryotae
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Cut-Off
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479 aa
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2417 27 4731239 caspase-10/d [Homo sapiens]
2161 27 1835779 Fas-associated death domain protein interleukin-1b-converting en
1155 27 4731237 caspase-10/c [Homo sapiens]
907 18 7619910 caspase-10 [Xenopus laevis]
768 27 2440071 MACH-alpha-1 [Homo sapiens]
766 27 1457959 FADD-homologous ICE/CED-3-like protease [Homo sapiens]
765 27 4583149 caspase 8 [Homo sapiens]
757 27 4379029 MACH-alpha-2 [Homo sapiens]
757 27 2429162 apoptotic caspase Mch5-beta [Homo sapiens]
747 22 3193167 caspase-8 [Mus musculus]
746 22 4138211 caspase-8 [Mus musculus]
734 22 9454380 caspase-8 [Rattus norvegicus]
716 27 1401352 apoptotic cysteine protease Mch5 isoform alpha [Homo sapiens]
631 16 8778118 caspase-8 [Danio rerio]
610 22 2462593 flice [Mus musculus]
578 18 7619906 caspase-8 [Xenopus laevis]
488 27 3928274 MACH-alpha-3 [Homo sapiens]
426 22 1245144 MCH3/SCA-2 [Mesocricetus auratus]
425 22 2094814 caspase-7 [Mus musculus]
425 22 1894917 Lice2 cysteine protease [Mus musculus]
424 22 1945546 Mch3 [Mus musculus]
423 27 1125073 ICE-LAP3 [Homo sapiens]
422 27 1894913 Lice2 beta cysteine protease [Homo sapiens]
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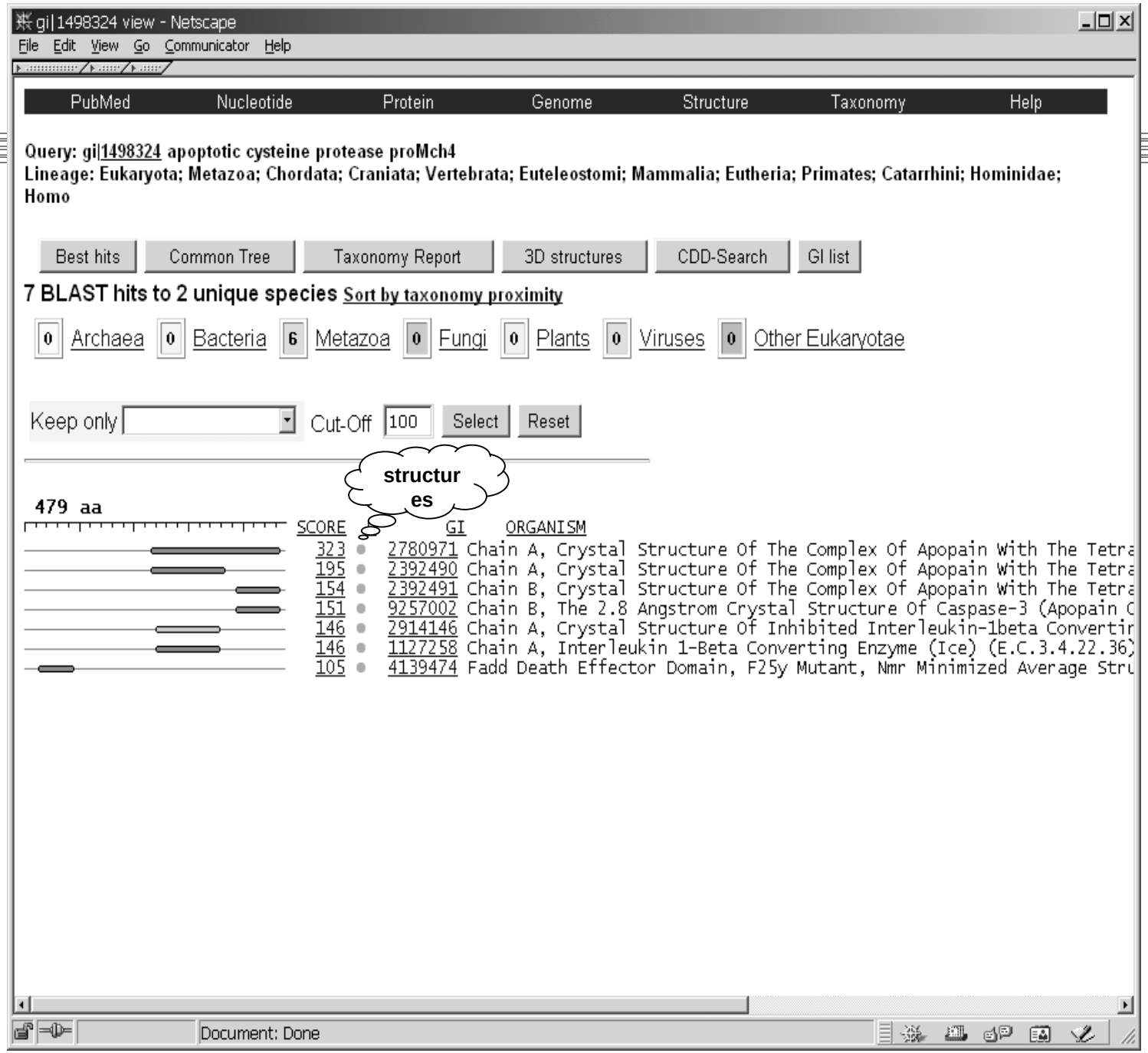
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0 Plants
0 Viruses
0 Other Eukaryotae
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100
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479 aa
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323 2780971 Chain A, Crystal Structure Of The Complex Of Apopain With The Tetra
195 2392490 Chain A, Crystal Structure Of The Complex Of Apopain With The Tetra
154 2392491 Chain B, Crystal Structure Of The Complex Of Apopain With The Tetra
151 9257002 Chain B, The 2.8 Angstrom Crystal Structure Of Caspase-3 (Apopain C
146 2914146 Chain A, Crystal Structure Of Inhibited Interleukin-1beta Convertir
146 1127258 Chain A, Interleukin 1-Beta Converting Enzyme (Ice) (E.C.3.4.22.36)
105 4139474 Fadd Death Effector Domain, F25y Mutant, Nmr Minimized Average Stru
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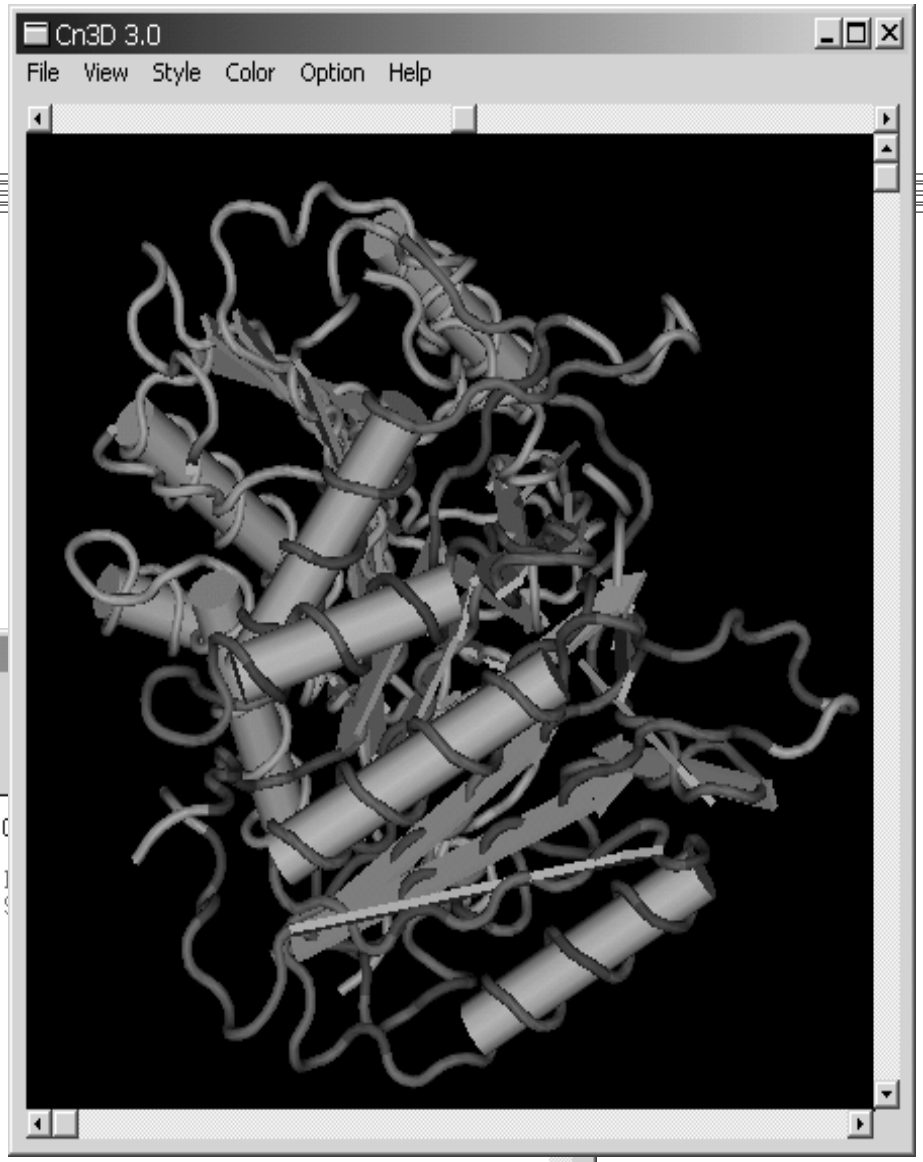
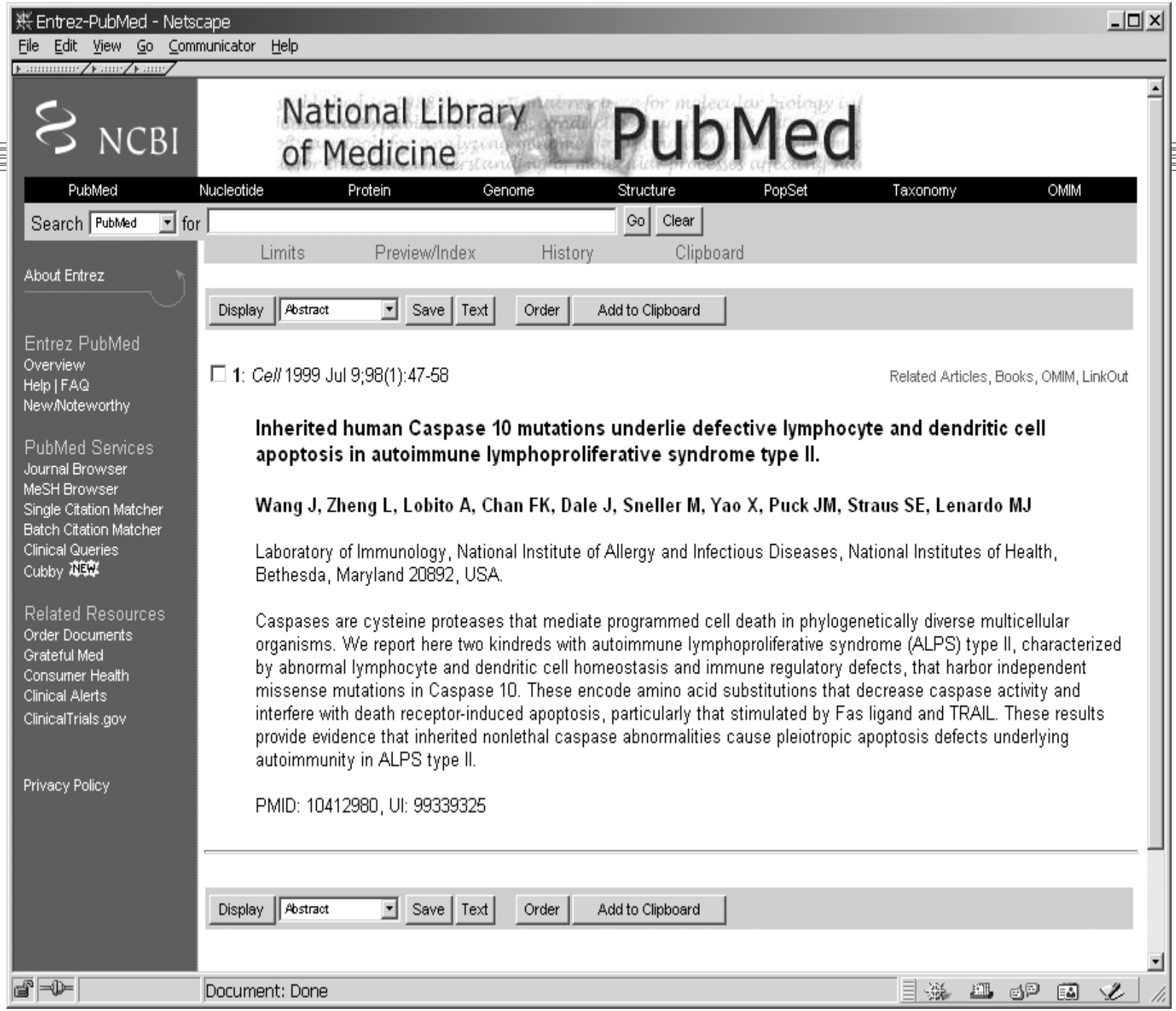
Structure of apopain (which has sequence similarity to caspase-10)

Sequence alignment of apopain and caspase-10



ALPS case study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1: Cell 1999 Jul 9;98(1):47-58
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Inherited human Caspase 10 mutations underlie defective lymphocyte and dendritic cell apoptosis in autoimmune lymphoproliferative syndrome type II.
Wang J, Zheng L, Lobito A, Chan FK, Dale J, Sneller M, Yao X, Puck JM, Straus SE, Lenardo MJ
Laboratory of Immunology, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland 20892, USA.
Caspases are cysteine proteases that mediate programmed cell death in phylogenetically diverse multicellular organisms. We report here two kindreds with autoimmune lymphoproliferative syndrome (ALPS) type II, characterized by abnormal lymphocyte and dendritic cell homeostasis and immune regulatory defects, that harbor independent missense mutations in Caspase 10. These encode amino acid substitutions that decrease caspase activity and interfere with death receptor-induced apoptosis, particularly that stimulated by Fas ligand and TRAIL. These results provide evidence that inherited nonlethal caspase abnormalities cause pleiotropic apoptosis defects underlying autoimmunity in ALPS type II.
PMID: 10412980, UI: 99339325
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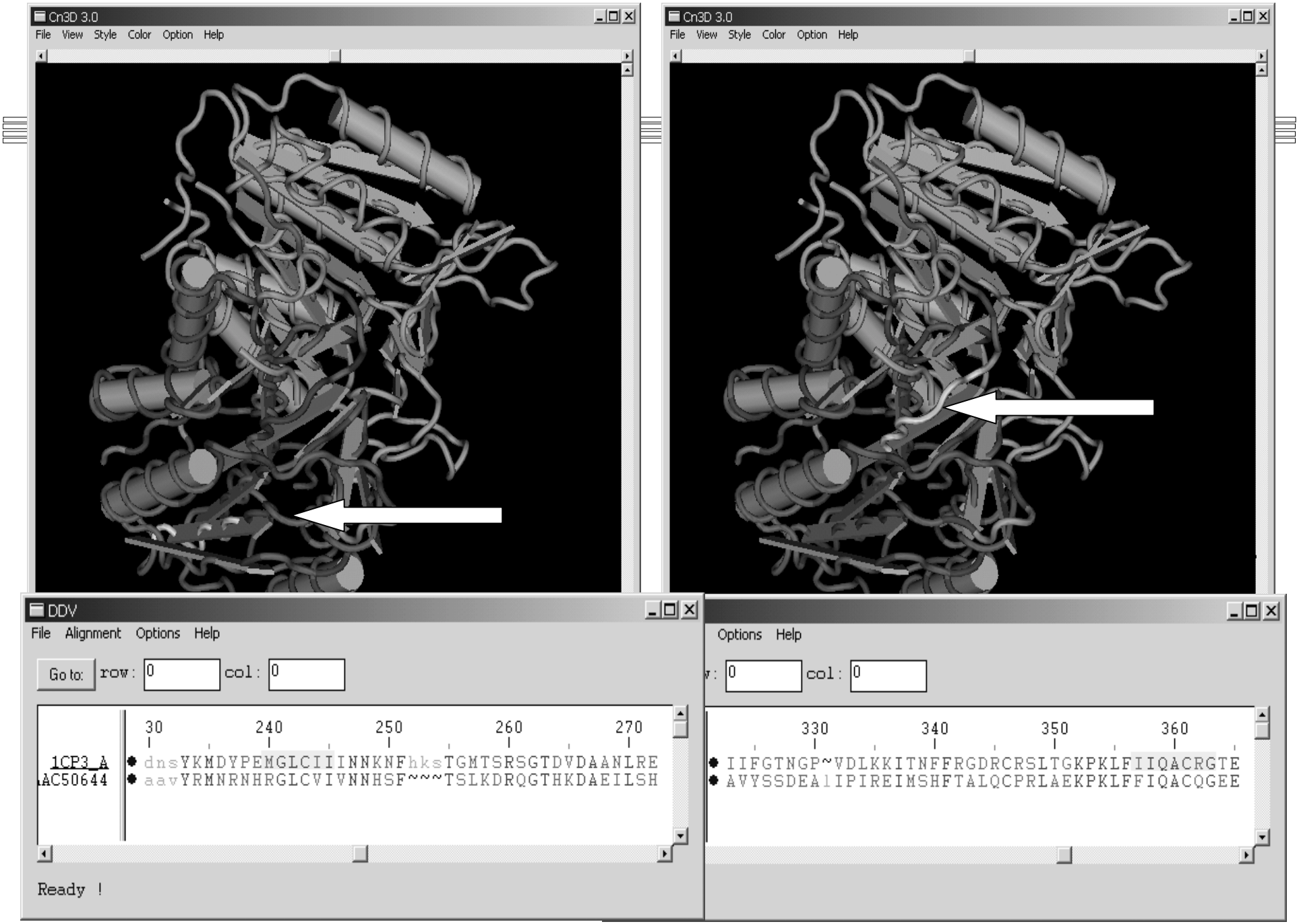
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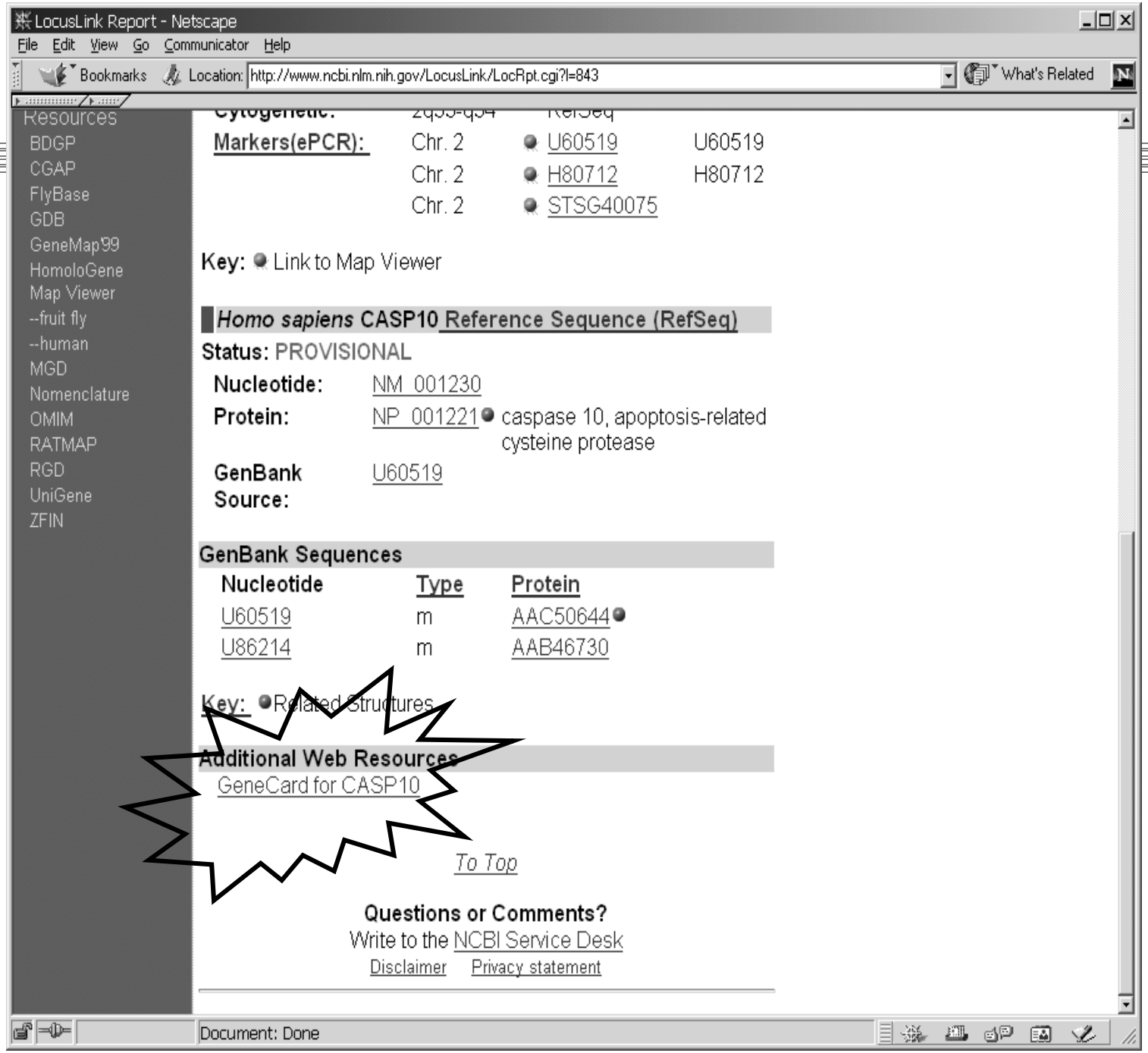
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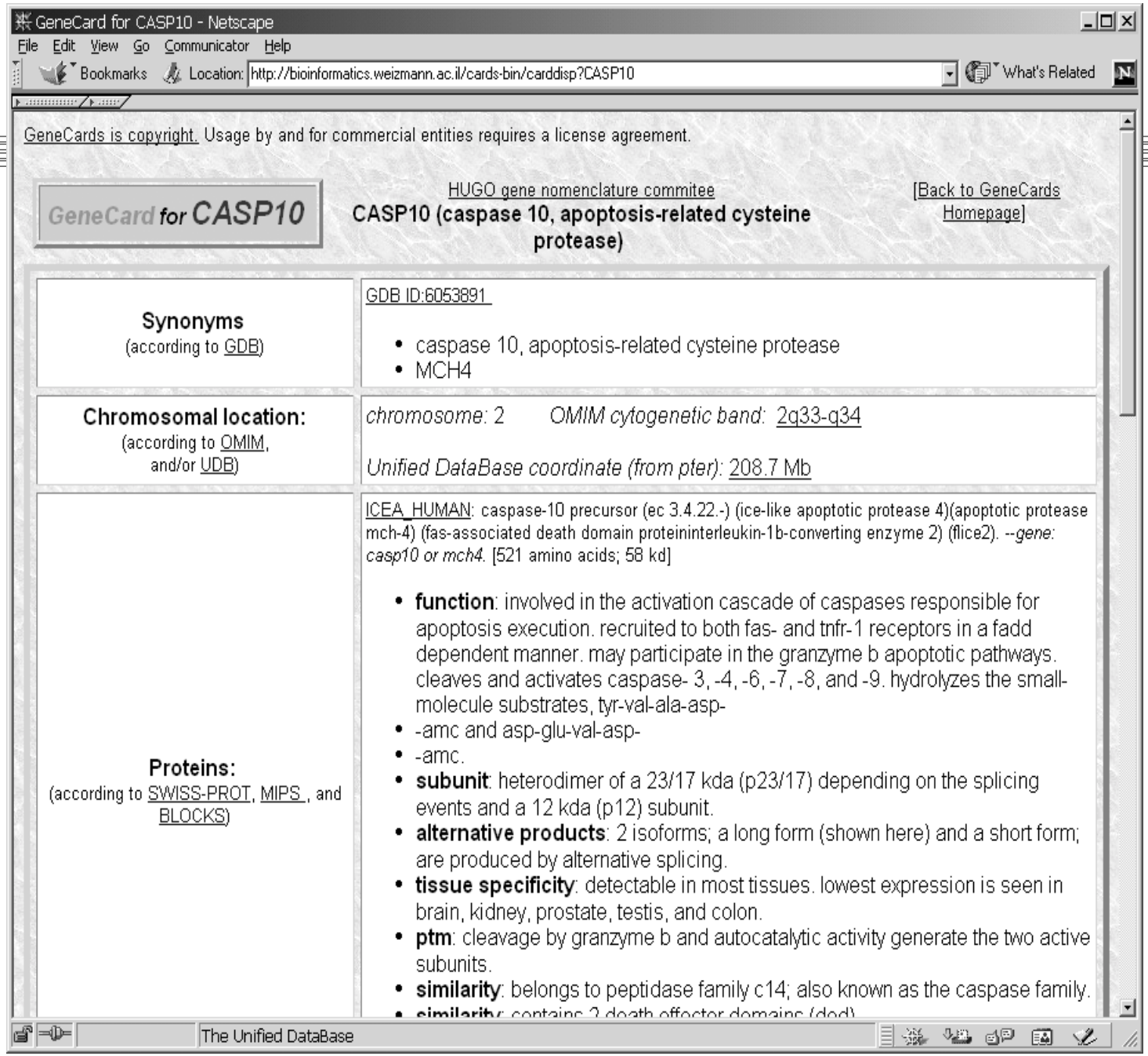
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CASP10 (caspase 10, apoptosis-related cysteine protease)
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Synonyms
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GDB ID:6053891
caspase 10, apoptosis-related cysteine protease
MCH4
Chromosomal location:
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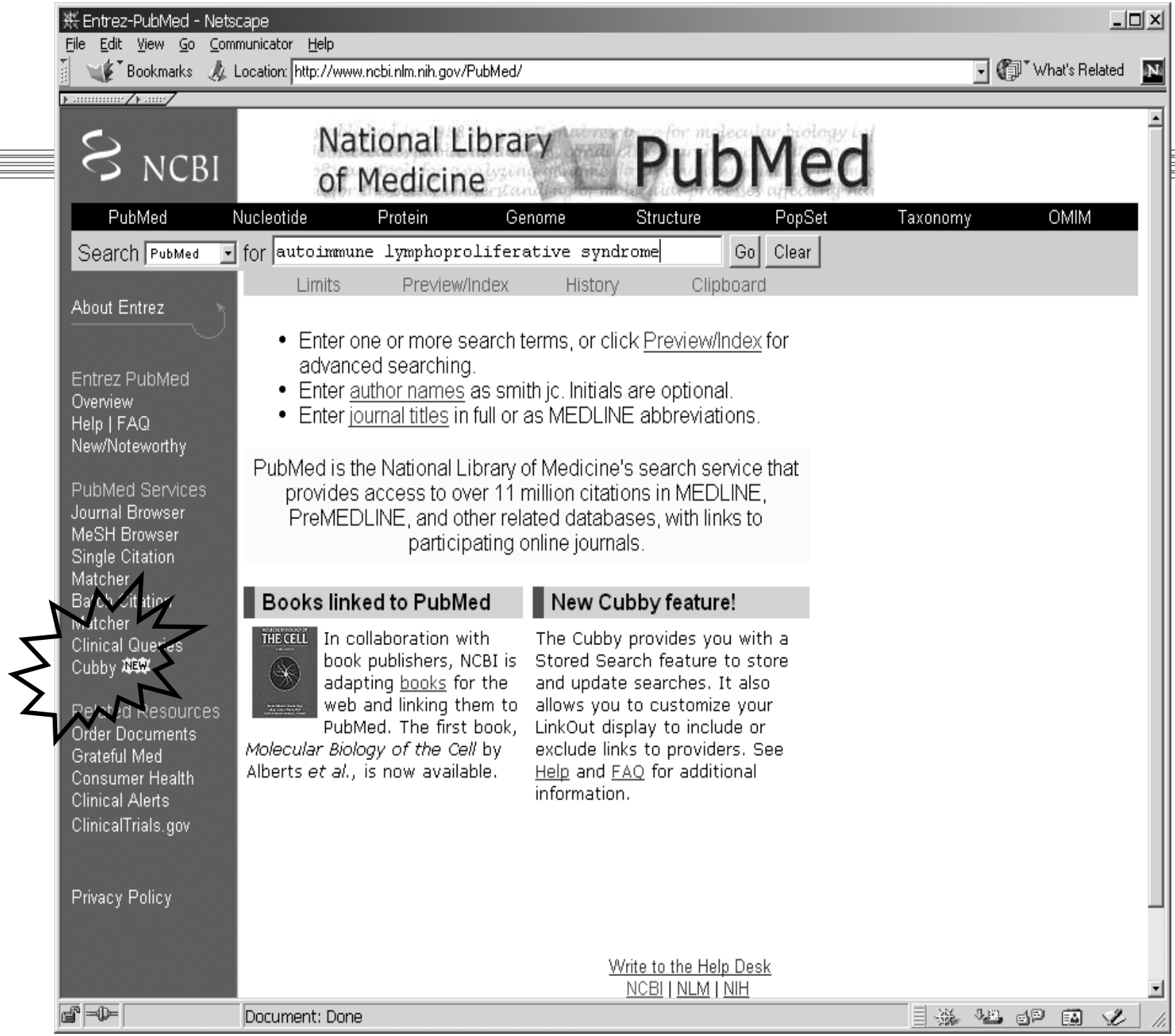
chromosome: 2 OMIM cytogenetic band: 2q33-q34
Unified DataBase coordinate (from pter): 208.7 Mb
Proteins:
(according to SWISS-PROT, MIPS, and BLOCKS)
ICEA_HUMAN: caspase-10 precursor (ec 3.4.22.-) (ice-like apoptotic protease 4)(apoptotic protease mch-4) (fas-associated death domain proteininterleukin-1b-converting enzyme 2) (flice2). --gene: casp10 or mch4. [521 amino acids; 58 kd]
function: involved in the activation cascade of caspases responsible for apoptosis execution. recruited to both fas- and tnfr-1 receptors in a fadd dependent manner. may participate in the granzyme b apoptotic pathways. cleaves and activates caspase- 3, -4, -6, -7, -8, and -9. hydrolyzes the small-molecule substrates, tyr-val-ala-asp-
-amc and asp-glu-val-asp-
-amc.
subunit: heterodimer of a 23/17 kda (p23/17) depending on the splicing events and a 12 kda (p12) subunit.
alternative products: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing.
tissue specificity: detectable in most tissues. lowest expression is seen in brain, kidney, prostate, testis, and colon.
ptm: cleavage by granzyme b and autocatalytic activity generate the two active subunits.
similarity: belongs to peptidase family c14; also known as the caspase family.
The Unified DataBase

The Cubby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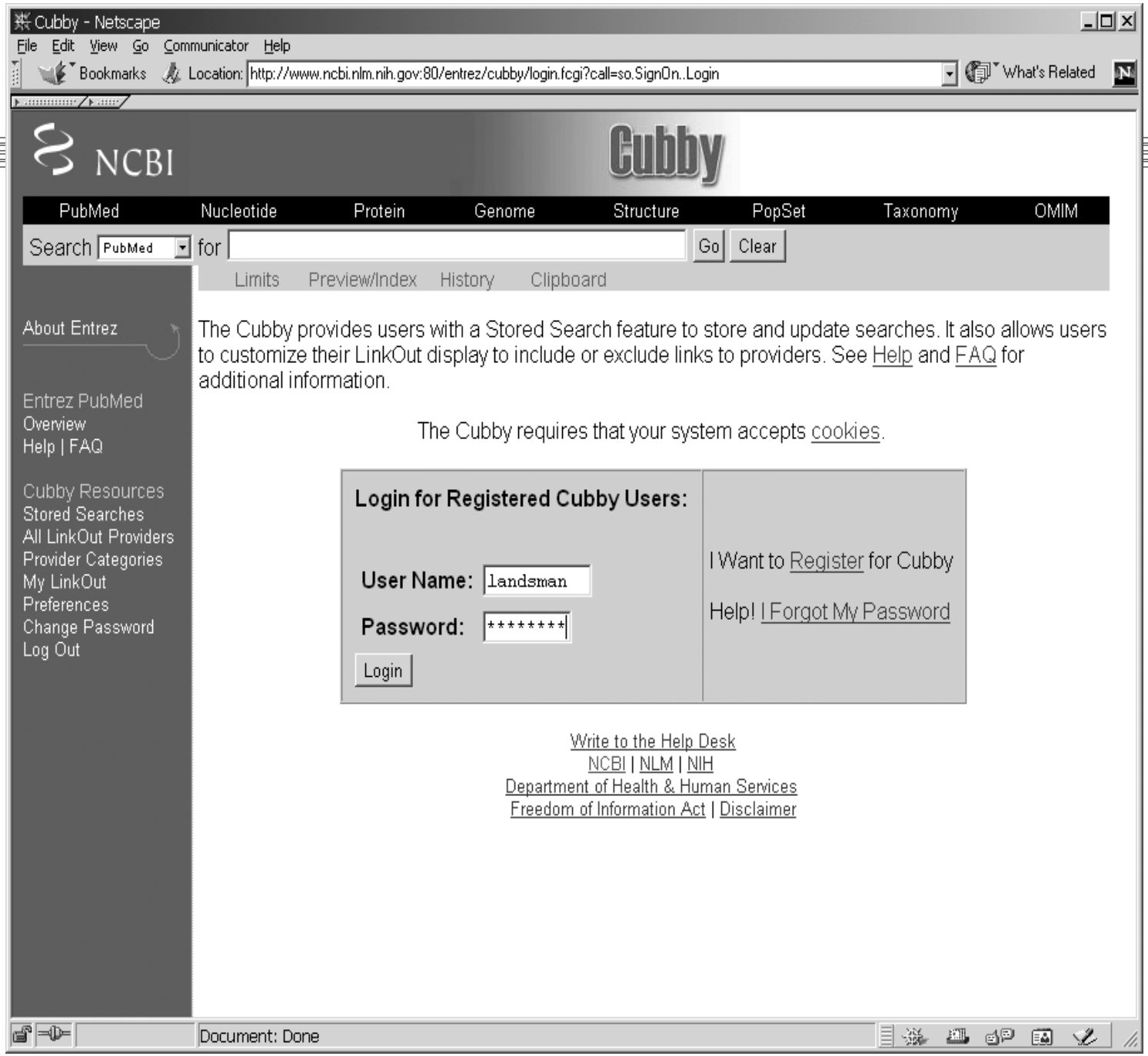
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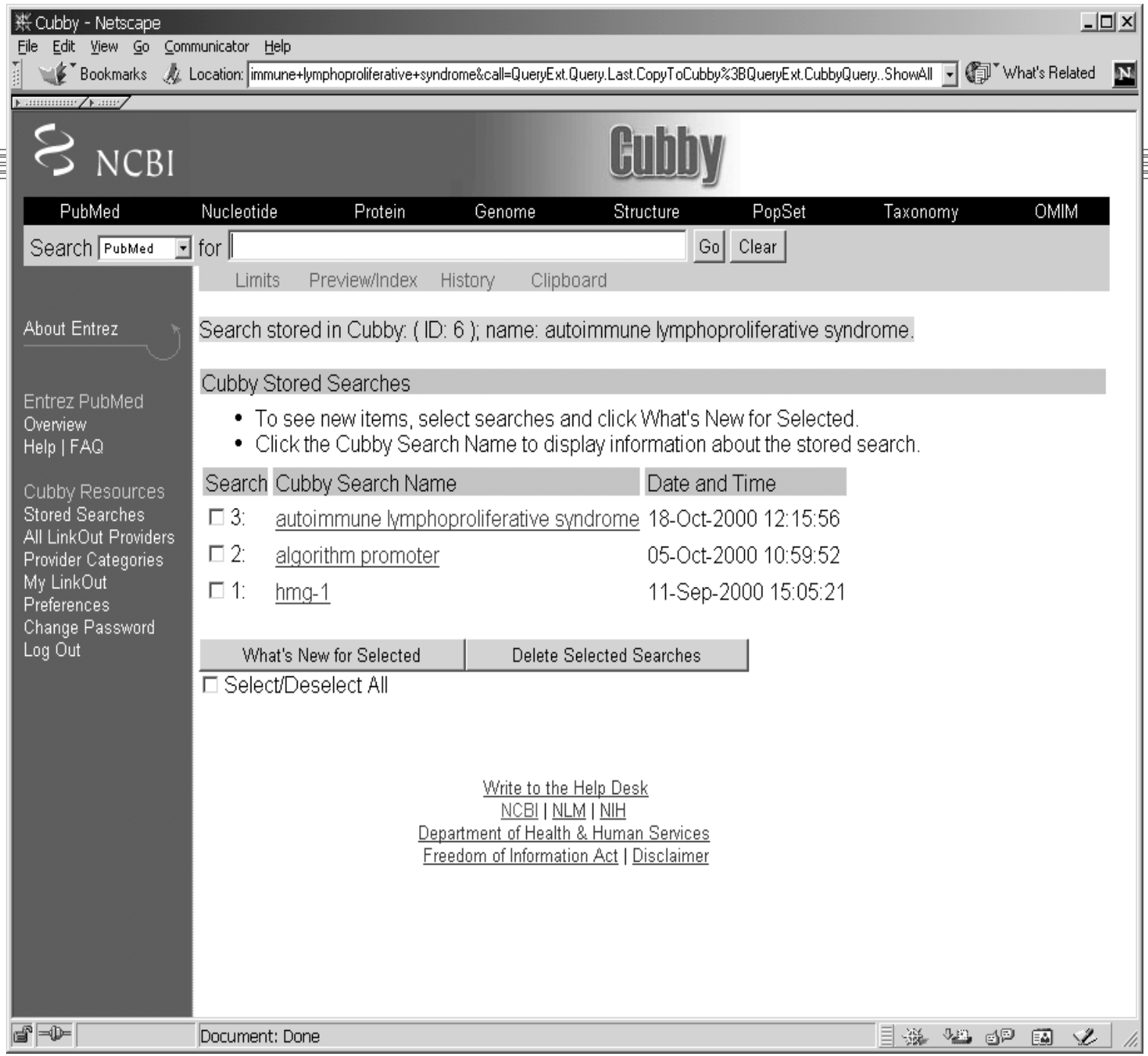
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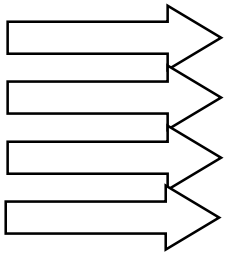
Help | FAQ
Cubby Resources
Stored Searches
All LinkOut Providers
Provider Categories
My LinkOut
Preferences
Change Password
Log Out
Search stored in Cubby: (ID: 6); name: autoimmune lymphoproliferative syndrome.
Cubby Stored Searches
To see new items, select searches and click What's New for Selected.
Click the Cubby Search Name to display information about the stored search.
Search Cubby Search Name Date and Time
3: autoimmune lymphoproliferative syndrome 18-Oct-2000 12:15:56
2: algorithm promoter 05-Oct-2000 10:59:52
1: hmg-1 11-Sep-2000 15:05:21
What's New for Selected Delete Selected Searches
Select/Deselect All
Write to the Help Desk
NCBI | NLM | NIH
Department of Health & Human Services
Freedom of Information Act | Disclaimer
Document: Done

More about querying



Entrez Home - Netscape

File Edit View Go Communicator Help

Bookmarks Location: http://www.ncbi.nlm.nih.gov/Entrez/ What's Related

NCBI

Entrez
search and retrieval system

PubMed Nucleotide Protein Genome Structure Popset Taxonomy OMIM

Search PubMed for Go Clear

PubMed
Protein
Nucleotide
Structure
Genome
PopSet
Taxonomy
OMIM

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About Ent

SITE MAP

PubMed Help
help documentation for PubMed

Entrez Help
help documentation for the rest of Entrez

The Entrez Databases
cross-references and information

Network Entrez
TCP/IP-based client-server version of WWW Entrez

Batch Entrez
retrieve a large number of sequences

Making WWW Links to Entrez
linking to PubMed and GenBank

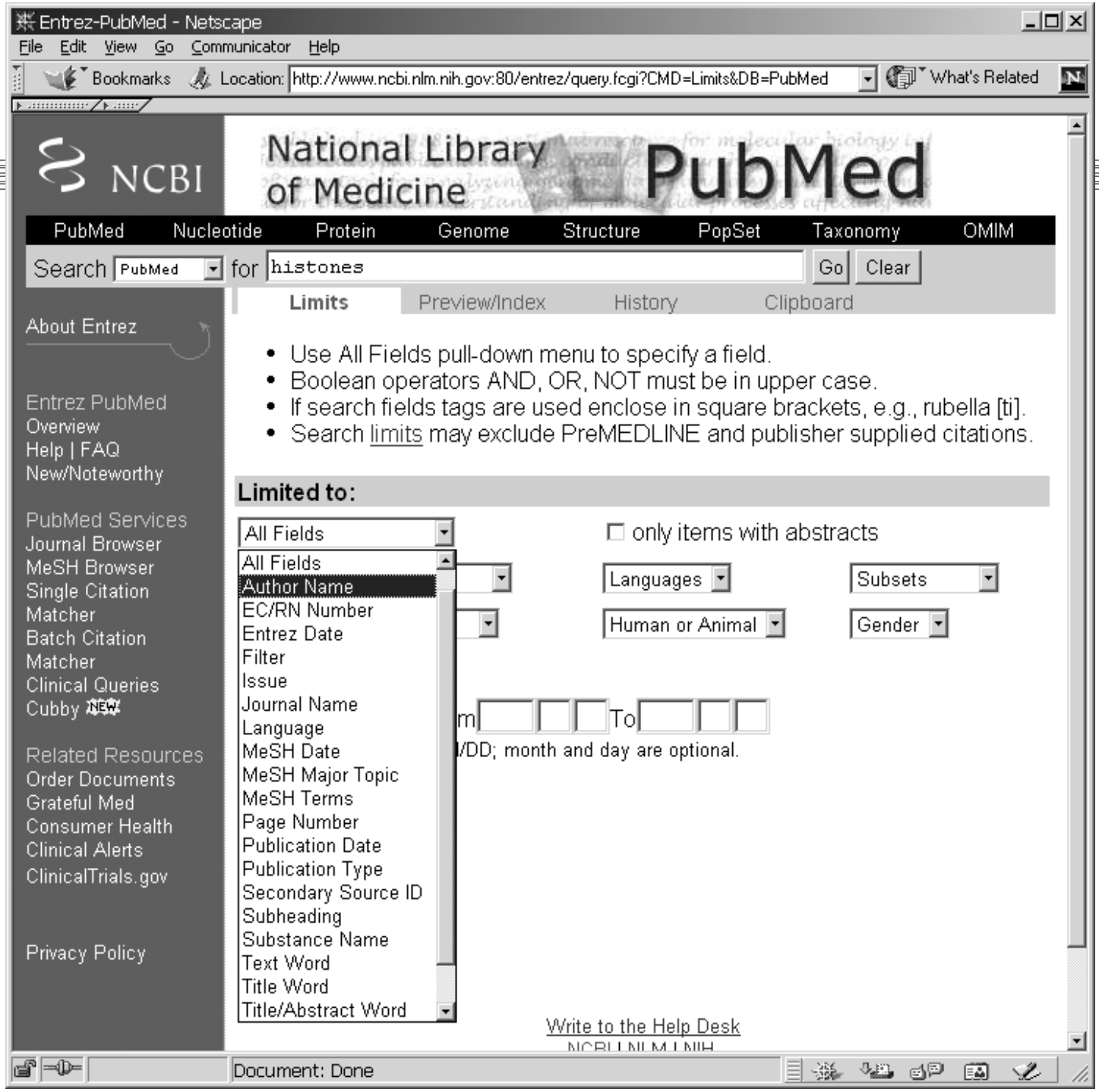
Entrez is a retrieval system for searching several linked databases.

It provides access to:

- PubMed: The biomedical literature (PubMed)
- Nucleotide sequence database (Genbank)
- Protein sequence database
- Structure: three-dimensional macromolecular structures
- Genome: complete genome assemblies
- PopSet: Population study data sets
- NEW Taxonomy: organisms in GenBank
- NEW OMIM: Online Mendelian Inheritance in Man

Pre-computed similarity searches are available for most database records producing a list of related sequences, structure neighbors, as well as related articles.

The Entrez search and retrieval system is provided by the National Center for Biotechnology Information. NCBI also builds, maintains, and distributes the GenBank sequence database.


Entrez-PubMed - Netscape
File Edit View Go Communicator Help
Bookmarks Location: http://www.ncbi.nlm.nih.gov:80/entrez/query.fcgi?CMD=Limits&DB=PubMed What's Related
NCBI
National Library of Medicine
PubMed
PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM
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Single Citation Matcher
Batch Citation Matcher
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Cubby NEW
Related Resources
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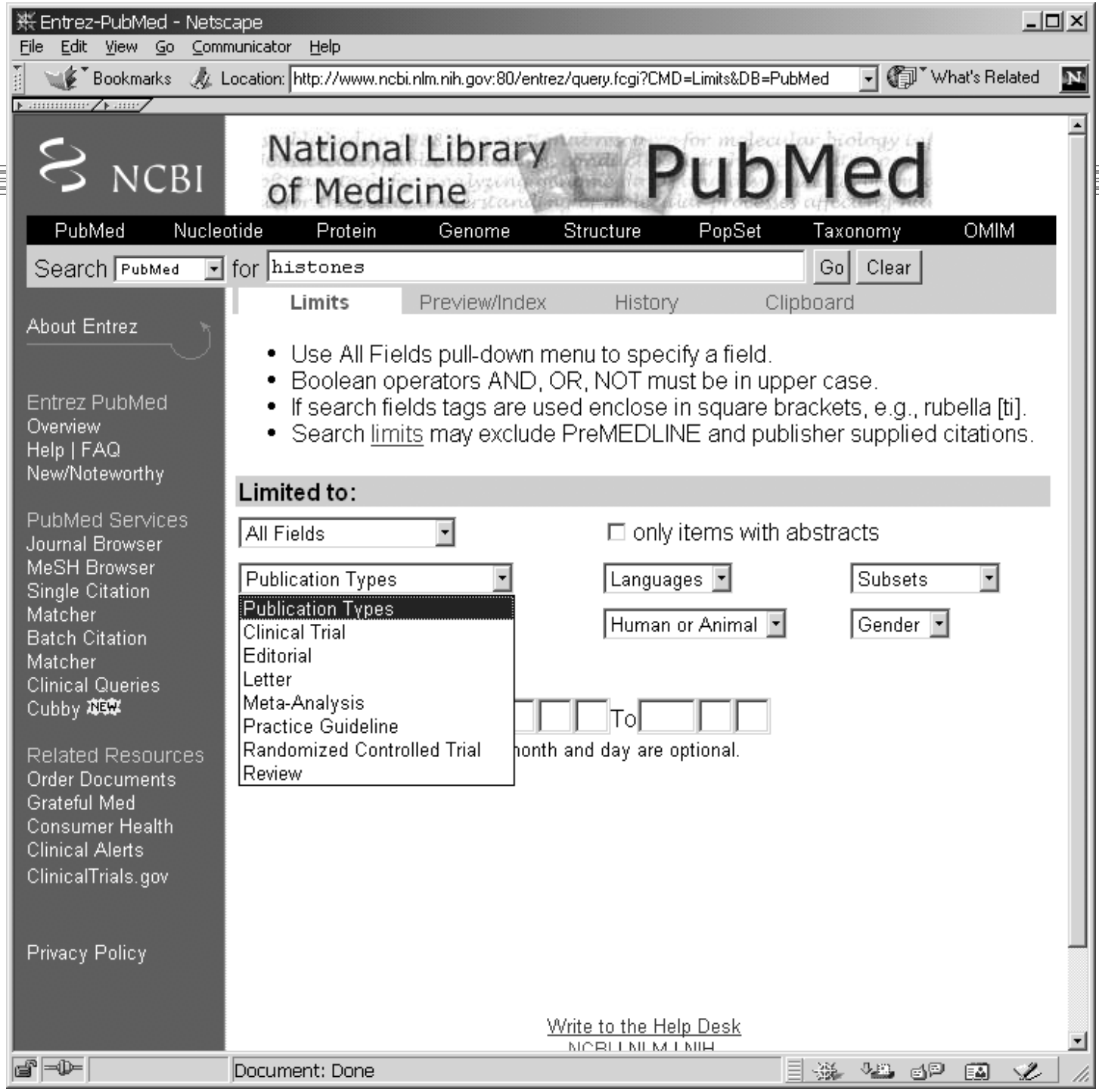
Grateful Med
Consumer Health
Clinical Alerts
ClinicalTrials.gov
Privacy Policy
Use All Fields pull-down menu to specify a field.
Boolean operators AND, OR, NOT must be in upper case.
If search fields tags are used enclose in square brackets, e.g., rubella [ti].
Search limits may exclude PreMEDLINE and publisher supplied citations.
Limited to:
All Fields
only items with abstracts
All Fields
Author Name
EC/RN Number
Entrez Date
Filter
Issue
Journal Name
Language
MeSH Date
MeSH Major Topic
MeSH Terms
Page Number
Publication Date
Publication Type
Secondary Source ID
Subheading
Substance Name
Text Word
Title Word
Title/Abstract Word
Languages
Subsets
Human or Animal
Gender
m To
/DD; month and day are optional.
Write to the Help Desk
Document: Done


Entrez-PubMed - Netscape
File Edit View Go Communicator Help
Bookmarks Location: http://www.ncbi.nlm.nih.gov:80/entrez/query.fcgi?CMD=Limits&DB=PubMed What's Related
NCBI
National Library of Medicine
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Batch Citation Matcher
Clinical Queries
Cubby NEW
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Grateful Med
Consumer Health
Clinical Alerts
ClinicalTrials.gov
Privacy Policy
Use All Fields pull-down menu to specify a field.
Boolean operators AND, OR, NOT must be in upper case.
If search fields tags are used enclose in square brackets, e.g., rubella [ti].
Search limits may exclude PreMEDLINE and publisher supplied citations.
Limited to:
All Fields
only items with abstracts
Publication Types
Languages
Subsets
Publication Types
Clinical Trial
Editorial
Letter
Meta-Analysis
Practice Guideline
Randomized Controlled Trial
Review
Human or Animal
Gender
To
onth and day are optional.
Write to the Help Desk
Document: Done

Entrez-Genome - Netscape

File Edit View Go Communicator Help

Bookmarks Location: http://www.ncbi.nlm.nih.gov:80/entrez/query.fcgi?db=Genome What's Related

NCBI

Entrez Genome

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search Genome for Go Clear

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About Entrez

Entrez Genomes Help

Submitting genome sequences

All Organisms

Prominent Organisms

Microbial genomes
Taxonomy Tree
BLAST
List of projects
PDB neighbors

Archaea
Genome
Plasmids

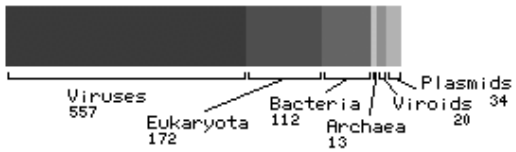
Bacteria
Genome
Plasmids

Eukaryota

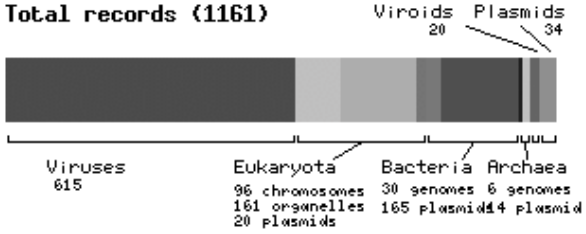
The whole genomes of over 800 organisms can be found in Entrez Genomes. The genomes represent both completely sequenced organisms and those for which sequencing is in progress. All three main domains of life - bacteria, archaea, and eukaryota - are represented, as well as many viruses and organelles.

Entrez Genomes statistics

Total species (908)



Total records (1161)



Latest complete genome: *Halobacterium*

Related Resources

Homo sapiens Map Viewer

Drosophila melanogaster sequence and resources

Microbial sequencing projects list

Organelle reference sequences and tools

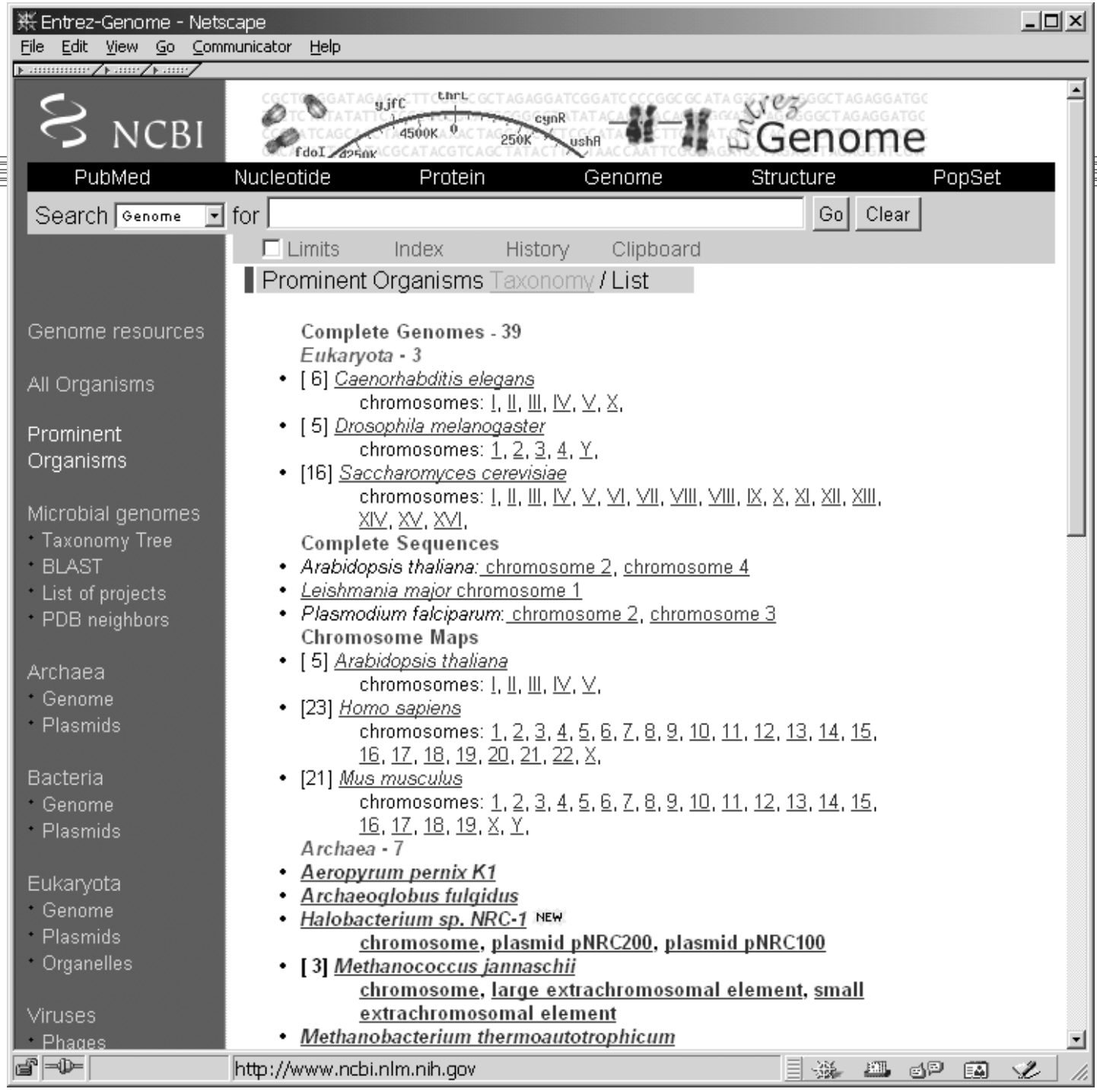
Malaria genetics and genomics

Retrovirus tools and resources

BLAST unfinished microbial genomes

COGs clusters of orthologous

Document: Done


Entrez-Genome - Netscape
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NCBI
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Prominent Organisms Taxonomy / List
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Plasmids
Bacteria
Genome
Plasmids
Eukaryota
Genome
Plasmids
Organelles
Viruses
Phages
Complete Genomes - 39
Eukaryota - 3
[6] Caenorhabditis elegans
chromosomes: I, II, III, IV, V, X,
[5] Drosophila melanogaster
chromosomes: 1, 2, 3, 4, Y,
[16] Saccharomyces cerevisiae
chromosomes: I, II, III, IV, V, VI, VII, VIII, VIII, IX, X, XI, XII, XIII, XIV, XV, XVI,
Complete Sequences
Arabidopsis thaliana: chromosome 2, chromosome 4
Leishmania major chromosome 1
Plasmodium falciparum: chromosome 2, chromosome 3
Chromosome Maps
[5] Arabidopsis thaliana
chromosomes: I, II, III, IV, V,
[23] Homo sapiens
chromosomes: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, X,
[21] Mus musculus
chromosomes: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, X, Y,
Archaea - 7
Aeropyrum pernix K1
Archaeoglobus fulgidus
Halobacterium sp. NRC-1 NEW
chromosome, plasmid pNRC200, plasmid pNRC100
[3] Methanococcus jannaschii
chromosome, large extrachromosomal element, small extrachromosomal element
Methanobacterium thermoautotrophicum
http://www.ncbi.nlm.nih.gov

Summary sequence view - Netscape

File Edit View Go Communicator Help

NCBI

Entrez Genome

BLAST PubMed Nucleotide Protein Genome Structure PopSet Taxonomy Help

Escherichia coli K-12 MG1655 complete genome

Accession: NC_000913
Total Bases: 4639221 bp
Completed: Oct 13, 1998.

Feature table:
Protein coding genes: 4289
Structural RNAs: 115

Distribution of BLAST protein homologs by:
COGs (Clusters of Orthologous Groups)
Taxa (Sequences grouped by superkingdom)
3D Structure (Sequences with known structure)

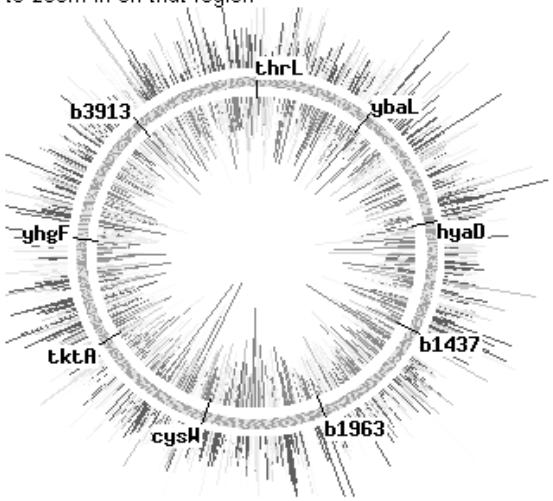
Contributor: U Wisc

You may download chromosome sequence data from NCBI FTP site

Start from : Go Search for gene Find

Protein coding genes distribution map

To see map locations of genes, click on a region in the map, to zoom in on that region



Gene Classification based on COG functional categories

- Translation, ribosomal structure and biogenesis
- Transcription
- DNA replication, recombination and repair
- Cell division and chromosome partitioning
- Posttranslational modification, protein turnover
- Cell envelope biogenesis, outer membrane
- Cell motility and secretion
- Inorganic ion transport and metabolism
- Signal transduction mechanisms
- Energy production and conversion
- Carbohydrate transport and metabolism
- Amino acid transport and metabolism
- Nucleotide transport and metabolism
- Coenzyme metabolism
- Lipid metabolism
- General function prediction only
- Function unknown
- No COG match

Document: Done

Saccharomyces cerevisiae genome - Netscape

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PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM Help

Search for on chromosome(s) Find

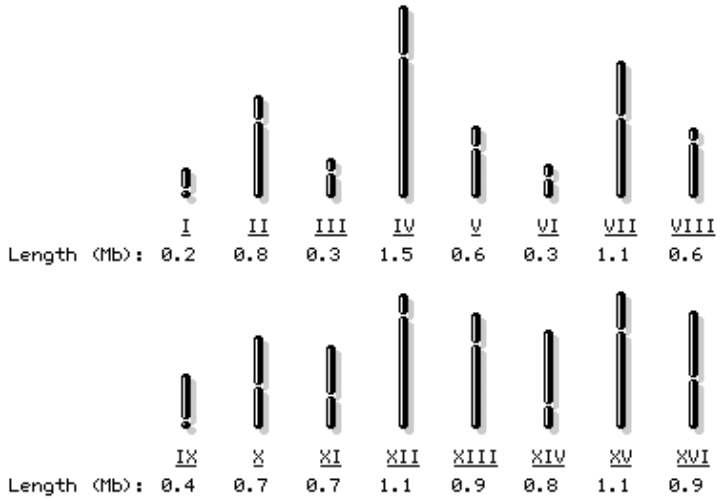
Entrez Genomes

Prominent organisms

FTP SITE

Related Databases:
SGD
MIPS
YPD

Saccharomyces cerevisiae genome



This collection of *Saccharomyces cerevisiae* complete chromosome sequences and annotations is a part of the NCBI Reference Sequence (RefSeq) project that provides curated sequence data and related information for the community to use as a standard. The nucleotide and protein sequences, and all other annotations, are provided by the Saccharomyces Genome Database (SGD) and will be revised as SGD is updated.

Document: Done

Structure searching ...

http://www.ncbi.nlm.nih.gov/Structure/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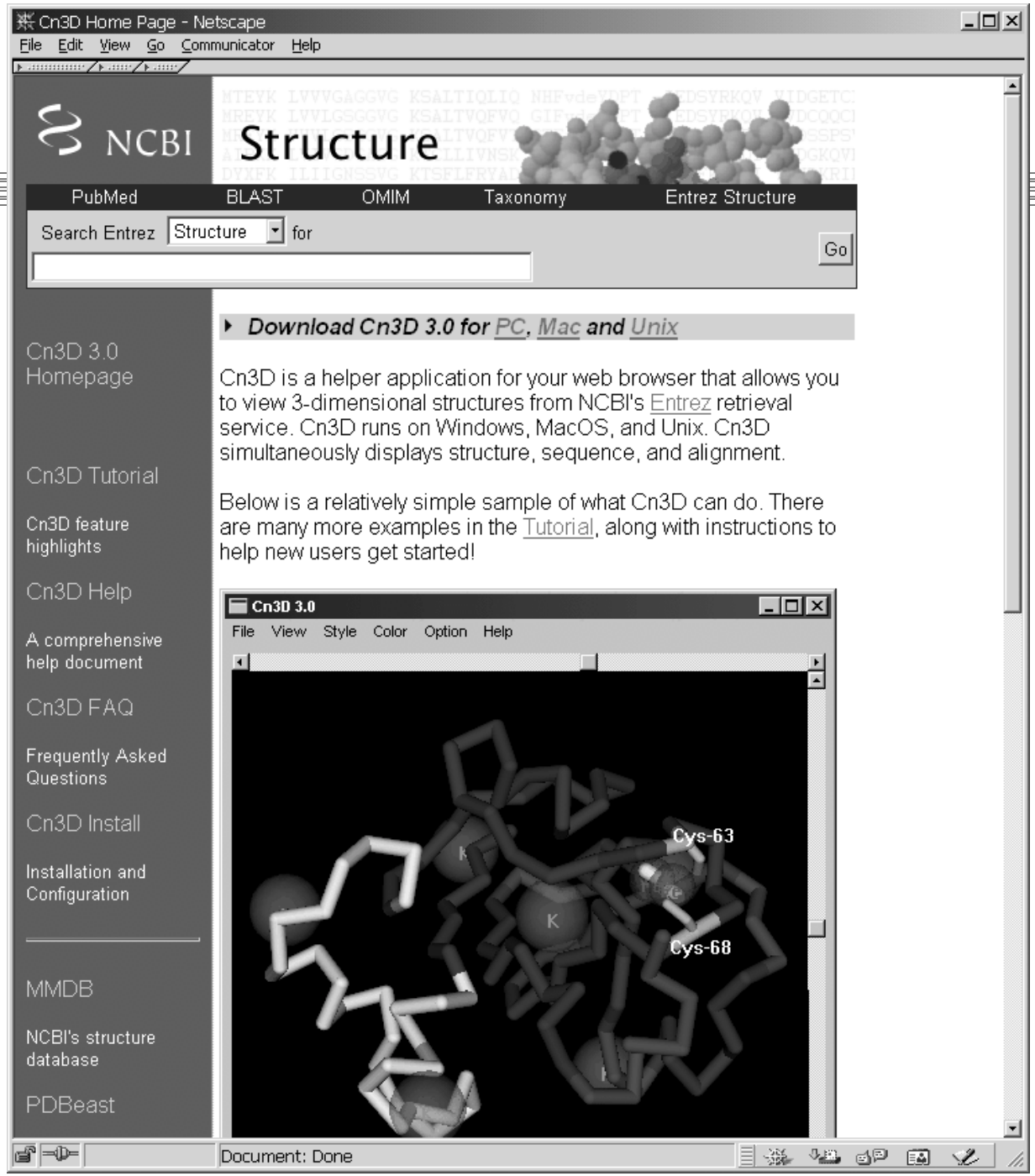
Structure Research
The NCBI Structure group
MMDB
About Entrez's structure database
PDBeast
Taxonomy in MMDB
Cn3D NEW
3D-structure viewer
VAST
Structure comparisons
VAST Search
Submit structure database searches
Research
Structure Group research projects
Hints on finding a Structure
To search by keyword, like "aconitase"
To search by protein sequence
To search by nucleotide sequence
New structure viewer
Cn3D is NCBI's 3D structure viewer. As a helper application for your web browser, it allows you to interactively view 3-D structures, sequences, and sequence alignments. Cn3D is available for Windows, MacOS, and Unix. More...
About the Database
The Molecular Modelling Database (MMDB) contains 3-D macromolecular structures, including proteins and polynucleotides. MMDB contains over 10,000 structures and is linked to the rest of the NCBI databases, including sequences, bibliographic citations, taxonomic classifications, and sequence and structure neighbors.
Document: Done


Cn3D Home Page - Netscape
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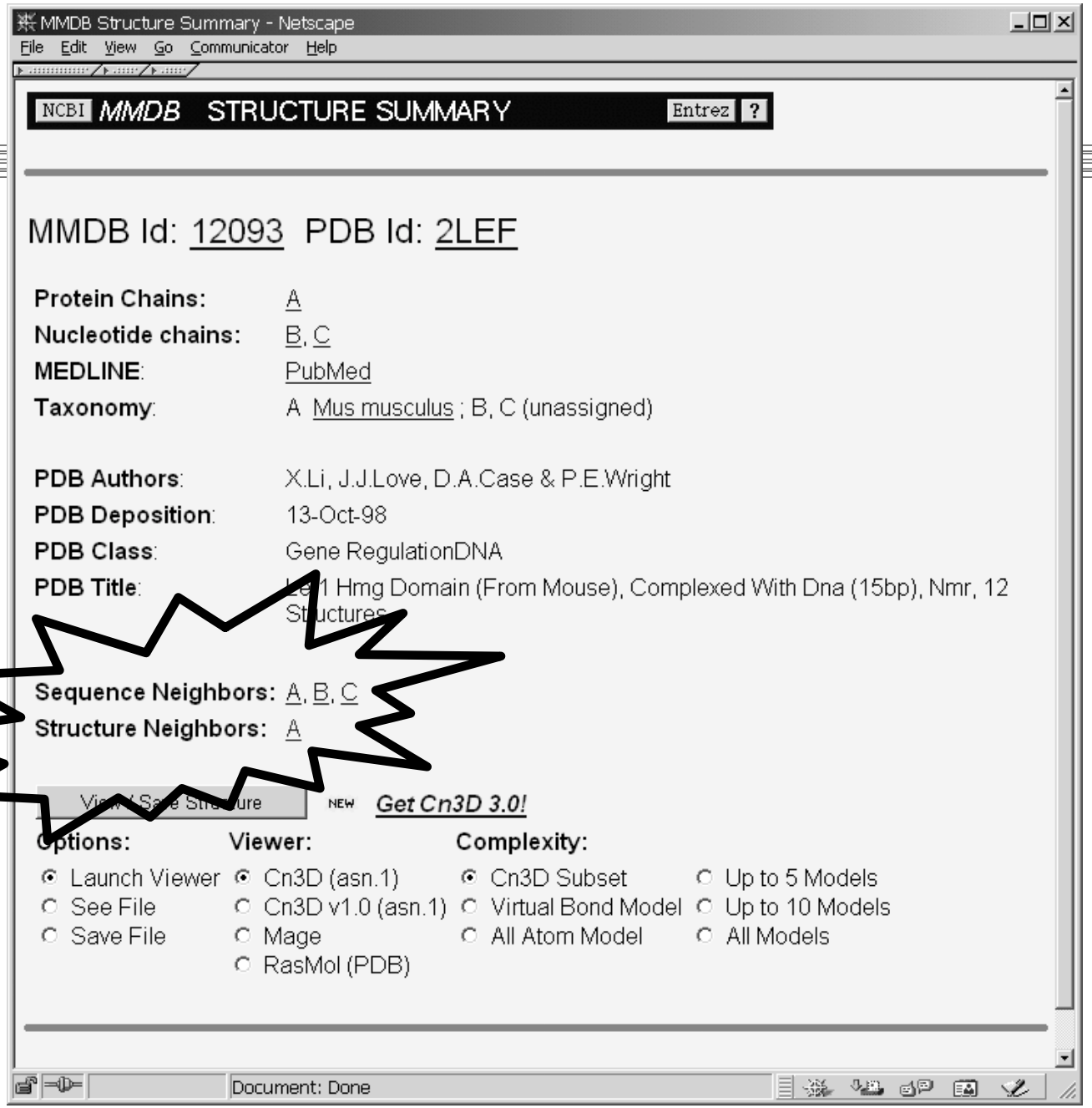
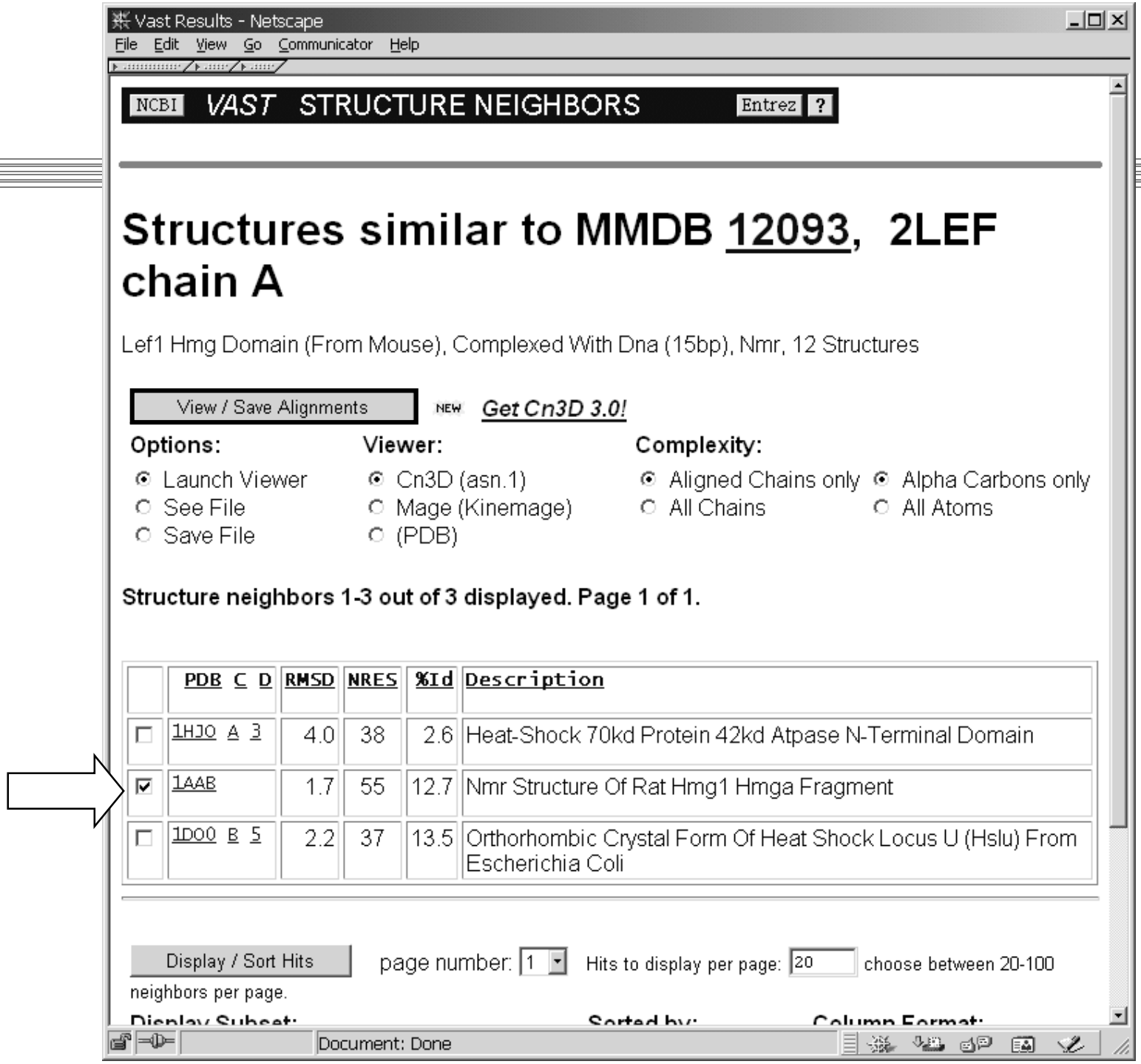
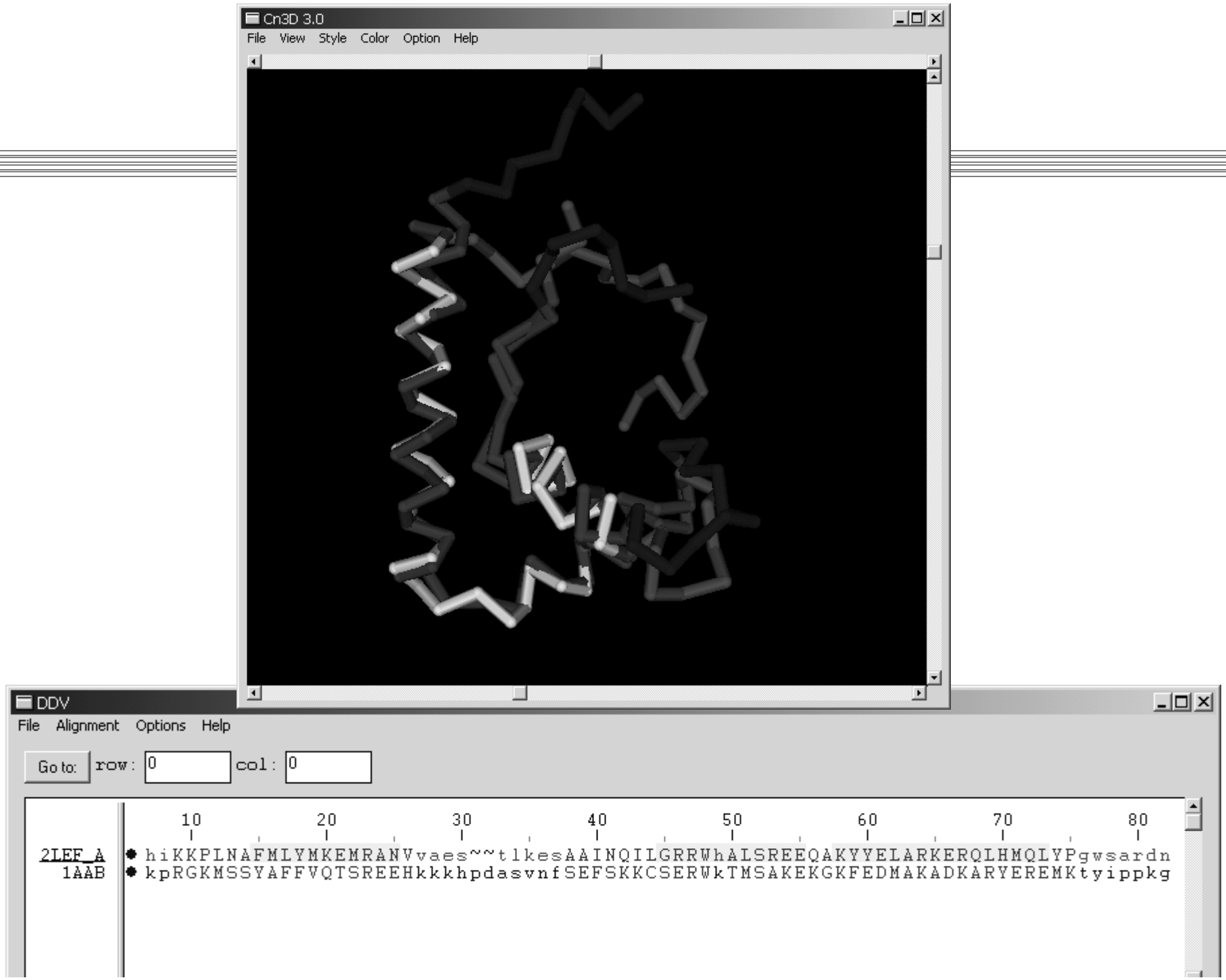
NCBI
Structure
PubMed BLAST OMIM Taxonomy Entrez Structure
Search Entrez Structure for
Go
Download Cn3D 3.0 for PC, Mac and Unix
Cn3D 3.0 Homepage
Cn3D Tutorial
Cn3D feature highlights
Cn3D Help
A comprehensive help document
Cn3D FAQ
Frequently Asked Questions
Cn3D Install
Installation and Configuration
MMDB
NCBI's structure database
PDBeast
Cn3D is a helper application for your web browser that allows you to view 3-dimensional structures from NCBI's Entrez retrieval service. Cn3D runs on Windows, MacOS, and Unix. Cn3D simultaneously displays structure, sequence, and alignment.
Below is a relatively simple sample of what Cn3D can do. There are many more examples in the Tutorial, along with instructions to help new users get started!
Cn3D 3.0
File View Style Color Option Help
Cys-63
Cys-68
Document: Done


MMDB Structure Summary - Netscape
File Edit View Go Communicator Help
NCBI MMDB STRUCTURE SUMMARY Entrez ?
MMDB Id: 12093 PDB Id: 2LEF
Protein Chains: A
Nucleotide chains: B, C
MEDLINE: PubMed
Taxonomy: A Mus musculus ; B, C (unassigned)
PDB Authors: X.Li, J.J.Love, D.A.Case & P.E.Wright
PDB Deposition: 13-Oct-98
PDB Class: Gene RegulationDNA
PDB Title: Lef1 Hmg Domain (From Mouse), Complexed With Dna (15bp), Nmr, 12 Structures
Sequence Neighbors: A, B, C
Structure Neighbors: A
NEW Get Cn3D 3.0!
Options: Launch Viewer See File Save File
Viewer: Cn3D (asn.1) Cn3D v1.0 (asn.1) Mage RasMol (PDB)
Complexity: Cn3D Subset Virtual Bond Model All Atom Model Up to 5 Models Up to 10 Models All Models
Document: Done


Vast Results - Netscape
File Edit View Go Communicator Help
NCBI VAST STRUCTURE NEIGHBORS Entrez ?
Structures similar to MMDB 12093, 2LEF chain A
Lef1 Hmg Domain (From Mouse), Complexed With Dna (15bp), Nmr, 12 Structures
View / Save Alignments
NEW Get Cn3D 3.0!
Options:
Launch Viewer
See File
Save File
Viewer:
Cn3D (asn.1)
Mage (Kinemage)
(PDB)
Complexity:
Aligned Chains only
All Chains
Alpha Carbons only
All Atoms
Structure neighbors 1-3 out of 3 displayed. Page 1 of 1.
PDB C D
RMSD
NRES
%Id
Description
1HJO A 3
4.0
38
2.6
Heat-Shock 70kd Protein 42kd Atpase N-Terminal Domain
1AAB
1.7
55
12.7
Nmr Structure Of Rat Hmg1 Hmga Fragment
1DO0 B 5
2.2
37
13.5
Orthorhombic Crystal Form Of Heat Shock Locus U (Hslu) From Escherichia Coli
Display / Sort Hits
page number: 1
Hits to display per page: 20
choose between 20-100 neighbors per page.
Document: Done


Cn3D 3.0
File View Style Color Option Help
DDV
File Alignment Options Help
Go to:
row :
0
col :
0
10 20 30 40 50 60 70 80
2LEF_A
1AAB
hiKKPLNAFMLYMKEMRANVvaes~~tlkesAAINQILGRRWhALSREEQAKYYELARKERQLHMQLYPgwsardn
kpRGKMSSYAFFVQTSREEHkkkhpdasvnfSEFSKKCSERWkTMSAKEKGKFEDMAKADKARYEREMKtyippkg